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## OM protein - protein search, using sw model

Run on: July 2, 2003, 19:20:50 ; Search time 23 Seconds

(without alignments)  
1609,901 Million cell updates/sec

Title: US-09-849-869A-16

Perfect score: 1661  
Sequence: 1 MDPTITLDELTPINGTEETLCYKOTLSLVTVTCIVSLVGLTGNVWVLMGLACRRKRRNA 60Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 440863 seqs, 114992915 residues

Total number of hits satisfying chosen parameters: 440863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB pep.\*
- 2: /cgn2\_6/ptodata/2/pubppaa/PTCTUS\_NEW\_PUB pep.\*
- 3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB pep.\*
- 4: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB pep.\*
- 5: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB pep.\*
- 6: /cgn2\_6/ptodata/2/pubppaa/PTCTUS\_PUBCOMB pep.\*
- 7: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB pep.\*
- 8: /cgn2\_6/ptodata/2/pubppaa/US09\_NEW\_PUB pep.\*
- 9: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB pep.\*
- 10: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB pep.\*
- 11: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB pep.\*
- 12: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB pep.\*
- 13: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB pep.\*
- 14: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1661	100.0	322	9	US-10-183-116-16
2	1661	100.0	322	9	US-10-079-384-4
3	1383	83.3	322	9	US-09-995-225-20
4	1383	83.3	322	9	US-10-183-116-31
5	1383	83.3	322	9	US-10-225-567A-674
6	1334	80.3	322	9	US-10-219-834-79
7	1294	77.9	322	9	US-09-995-225-18
8	1294	77.9	322	9	US-10-183-116-33
9	1294	77.9	322	9	US-10-225-567A-689
10	1212	73.0	328	9	US-10-219-834-20
11	1038.5	62.5	330	9	US-10-183-116-18
12	1038.5	62.5	330	9	US-10-079-384-12
13	1038.5	62.5	330	9	US-10-225-567A-649
14	1038.5	62.5	330	10	US-09-826-508-12
15	1038.5	62.5	330	10	US-09-750-373-24
16	1038.5	62.5	330	10	US-09-920-068A-4
17	1032	61.0	330	9	US-09-800-321A-31
18	1013.5	59.2	324	9	US-10-012-140-8
19	984	59.2	324	9	US-09-782-974C-58

20	821	49.4	338	9	US-10-183-116-41	Sequence 41, App1
21	779	46.9	273	9	US-10-183-116-85	Sequence 85, App1
22	773.5	46.6	325	10	US-09-920-068A-3	Sequence 3, App1
23	769.5	46.3	338	9	US-10-183-116-39	Sequence 39, App1
24	764.5	46.0	303	9	US-10-183-116-53	Sequence 53, App1
25	756.5	45.5	304	9	US-10-183-116-2	Sequence 2, App1
26	748.5	45.1	305	9	US-10-183-116-57	Sequence 57, App1
27	745.5	44.9	270	9	US-10-183-116-87	Sequence 87, App1
28	735	44.3	302	9	US-10-183-116-6	Sequence 6, App1
29	731.5	44.0	301	9	US-10-183-116-23	Sequence 23, App1
30	725	43.6	321	9	US-10-183-116-45	Sequence 45, App1
31	716.5	43.1	305	9	US-10-183-116-25	Sequence 11, App1
32	716.5	43.1	305	9	US-10-183-116-63	Sequence 25, App1
33	699.5	42.1	305	9	US-10-183-116-27	Sequence 63, App1
34	695	41.8	331	10	US-09-920-068A-1	Sequence 27, App1
35	692.5	41.7	332	9	US-10-183-116-47	Sequence 47, App1
36	687.5	41.4	268	9	US-10-183-116-79	Sequence 79, App1
37	682.5	41.1	305	9	US-10-183-116-12	Sequence 12, App1
38	680.5	41.0	305	9	US-10-183-116-65	Sequence 4, App1
39	679	40.9	300	9	US-10-183-116-67	Sequence 65, App1
40	678.5	40.8	303	9	US-10-183-116-21	Sequence 67, App1
41	675	40.6	287	9	US-10-183-116-21	Sequence 21, App1
42	672	40.5	304	9	US-10-183-116-73	Sequence 73, App1
43	671.5	40.4	282	9	US-10-183-116-55	Sequence 55, App1
44	667.5	40.2	305	9	US-10-183-116-59	Sequence 59, App1

## ALIGNMENTS

## RESULT 1

US-10-183-116-16  
; Sequence 16, Application US/10183116  
; Publication No. US2003092035A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David J.  
; APPLICANT: Dong, Xinzhang  
; APPLICANT: Zylka, Mark  
; APPLICANT: Simon, Melvin  
; APPLICANT: Han, Sang-Kyu  
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES  
; FILE REFERENCE: CALTE 4C1CPI  
; CURRENT APPLICATION NUMBER: US/10/183, 116  
; CURRENT FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: US 60/222,344  
; PRIOR FILING DATE: 2000-08-01  
; PRIOR APPLICATION NUMBER: US 60/202,027  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 09/704,707  
; PRIOR FILING DATE: 2000-11-03  
; PRIOR APPLICATION NUMBER: US 60/285,493  
; PRIOR FILING DATE: 2001-04-19  
; PRIOR APPLICATION NUMBER: US 09/849,869  
; PRIOR FILING DATE: 2001-05-04  
; NUMBER OF SEQ ID NOS: 109  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-183-116-16

Query Match 100.0%; Score 1661; DB 9; Length 322;  
Best Local Similarity 100.0%; Pred. No. 4,9e-142;  
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPTITLDELTPINGTEETLCYKOTLSLVTVTCIVSLVGLTGNVWVLMGLACRRKRRNA 60  
Db 1 MDPTITLDELTPINGTEETLCYKOTLSLVTVTCIVSLVGLTGNVWVLMGLACRRKRRNA 60  
QY 61 FSYIINLAADPLFISGRLLYSLSFISPTISKILYVPMVFSYFAGISPLSAVSTER 120

Db 61 FSIYILNLAADFLFLSGRLIYSLISFISIPHTISKILYPMWMSYFAGLSFLSAVSTER 120  
QY 121 CLSVLMPITWYRCHRPETHLSAVVAVCVLWALSLRSLTLEMMCGFLFSGADSAMCOTSPFIT 180  
Db 121 CLSVLMPITWYRCHRPETHLSAVVAVCVLWALSLRSLTLEMMCGFLFSGADSAMCOTSPFIT 180  
QY 181 VAMLIPLFCVVLGSSSLVLLIRILGSKRIPLTRLYVTLLTVLVEFLGCLPFGIOFPLFL 240  
Db 181 VAMLIPLFCVVLGSSSLVLLIRILGSKRIPLTRLYVTLLTVLVEFLGCLPFGIOFPLFL 240  
QY 241 WIHVDREVLFCGHVHLSIFLSALNSSANPIIYFVGSFRORONKLVQALQDASE 300  
Db 241 WIHVDREVLFCGHVHLSIFLSALNSSANPIIYFVGSFRORONKLVQALQDASE 300  
QY 301 VDEGGGQLPEETLELSSGRLEQ 322  
Db 301 VDEGGGQLPEETLELSSGRLEQ 322

## RESULT 2

US-10-079-384-4  
; Sequence 4, Application US/10079384  
; Publication No. US20030108986A1  
; GENERAL INFORMATION:  
; APPLICANT: Communi, Didier  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: 9409/2132  
; CURRENT APPLICATION NUMBER: US/10/079,384  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 09/885,453  
; PRIOR FILING DATE: 2001-06-20  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-079-384-4

Query Match 100.0%; Score 1661; DB 9; Length 322;  
Best Local Similarity 100.0%; Pred. No. 4,9e-142; Indels 0; Gaps 0;  
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDPTISTDLTLPINGTEETLCYKQTLSTVLCTIVSLVGLTGNAAVWMLGCRM RNA 60  
Db 1 MDPTISTDLTLPINGTEETLCYKQTLSTVLCTIVSLVGLTGNAAVWMLGCRM RNA 60  
QY 61 FSIYILNLAADFLFLSGRLIYSLISFISIPHTISKILYPMWMSYFAGLSFLSAVSTER 120  
Db 61 FSIYILNLAADFLFLSGRLIYSLISFISIPHTISKILYPMWMSYFAGLSFLSAVSTER 120  
QY 121 CLSVLMPITWYRCHRPETHLSAVVAVCVLWALSLRSLTLEMMCGFLFSGADSAMCOTSPFIT 180  
Db 121 CLSVLMPITWYRCHRPETHLSAVVAVCVLWALSLRSLTLEMMCGFLFSGADSAMCOTSPFIT 180  
QY 181 VAMLIPLFCVVLGSSSLVLLIRILGSKRIPLTRLYVTLLTVLVEFLGCLPFGIOFPLFL 240  
Db 181 VAMLIPLFCVVLGSSSLVLLIRILGSKRIPLTRLYVTLLTVLVEFLGCLPFGIOFPLFL 240  
QY 241 WIHVDREVLFCGHVHLSIFLSALNSSANPIIYFVGSFRORONKLVQALQDASE 300  
Db 241 WIHVDREVLFCGHVHLSIFLSALNSSANPIIYFVGSFRORONKLVQALQDASE 300  
QY 301 VDEGGGQLPEETLELSSGRLEQ 322  
Db 301 VDEGGGQLPEETLELSSGRLEQ 322

RESULT 3  
US-09-995-225-20  
; Sequence 20, Application US/09995225  
; Publication No. US20020193584A1  
; GENERAL INFORMATION:

APPLICANT: Chen, Ruoping  
APPLICANT: Chu, Zhi Liang  
APPLICANT: Dang, Huang T.  
APPLICANT: Lowitz, Kevin P.  
APPLICANT: Pride, Cameron  
TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G  
FILE REFERENCE: AREN-0308  
CURRENT APPLICATION NUMBER: US/09/995,225  
CURRENT FILING DATE: 2001-11-26  
PRIOR APPLICATION NUMBER: 09/170,496  
PRIOR FILING DATE: 1998-10-13  
PRIOR APPLICATION NUMBER: PCT/US99/23938  
PRIOR FILING DATE: 1998-10-13  
PRIOR APPLICATION NUMBER: 60/253,404  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/255,366  
PRIOR FILING DATE: 2000-12-12  
PRIOR APPLICATION NUMBER: 60/270,286  
PRIOR FILING DATE: 2001-02-20  
PRIOR APPLICATION NUMBER: 60/282,365  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: 60/270,266  
PRIOR FILING DATE: 2001-02-20  
PRIOR APPLICATION NUMBER: 60/282,032  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: 60/282,358  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: 60/282,356  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: 60/290,917  
PRIOR FILING DATE: 2001-05-14  
PRIOR APPLICATION NUMBER: 60/309,208  
PRIOR FILING DATE: 2001-07-31  
NUMBER OF SEQ ID NOS: 67  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 20  
LENGTH: 322  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: No. US20020193584A1e1 Sequence  
US-09-995-225-20

Query Match 83.3%; Score 1383; DB 9; Length 322;  
Best Local Similarity 83.5%; Pred. No. 5,8e-117; Indels 0; Gaps 0;  
Matches 269; Conservative 16; Mismatches 37; Indels 0; Gaps 0;  
QY 1 MDPTISTDLTLPINGTEETLCYKQTLSTVLCTIVSLVGLTGNAAVWMLGCRM RNA 60  
Db 1 MDPTISTDLTLPINGTEETLCYKQTLSTVLCTIVSLVGLTGNAAVWMLGCRM RNA 60  
QY 61 FSIYILNLAADFLFLSGRLIYSLISFISIPHTISKILYPMWMSYFAGLSFLSAVSTER 120  
Db 61 FSIYILNLAADFLFLSGRLIYSLISFISIPHTISKILYPMWMSYFAGLSFLSAVSTER 120  
QY 121 CLSVLMPITWYRCHRPETHLSAVVAVCVLWALSLRSLTLEMMCGFLFSGADSAMCOTSPFIT 180  
Db 121 CLSVLMPITWYRCHRPETHLSAVVAVCVLWALSLRSLTLEMMCGFLFSGADSAMCOTSPFIT 180  
QY 181 VAMLIPLFCVVLGSSSLVLLIRILGSKRIPLTRLYVTLLTVLVEFLGCLPFGIOFPLFL 240  
Db 181 VAMLIPLFCVVLGSSSLVLLIRILGSKRIPLTRLYVTLLTVLVEFLGCLPFGIOFPLFL 240  
QY 241 WIHVDREVLFCGHVHLSIFLSALNSSANPIIYFVGSFRORONKLVQALQDASE 300  
Db 241 WIHVDREVLFCGHVHLSIFLSALNSSANPIIYFVGSFRORONKLVQALQDASE 300  
QY 301 VDEGGGQLPEETLELSSGRLEQ 322  
Db 301 VDEGGGQLPEETLELSSGRLEQ 322

RESULT 4  
US-10-183-116-31  
; Sequence 31, Application US/10183116  
; Publication No. US20030092035A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, David J.  
; APPLICANT: Dong, Xinzhang  
; APPLICANT: Zylka, Mark  
; APPLICANT: Simon, Melvin  
; APPLICANT: Han, Sang-kyou  
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES  
; FILE REFERENCE: CALTE.4C1CPI  
; CURRENT APPLICATION NUMBER: US/10/183,116  
; CURRENT FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: US 60/222,344  
; PRIOR FILING DATE: 2000-08-01  
; PRIOR APPLICATION NUMBER: US 60/202,027  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 09/704,707  
; PRIOR FILING DATE: 2000-11-03  
; PRIOR APPLICATION NUMBER: US 60/285,493  
; PRIOR FILING DATE: 2001-04-19  
; PRIOR APPLICATION NUMBER: US 09/849,869  
; PRIOR FILING DATE: 2001-05-04  
; NUMBER OF SEQ ID NOS: 109  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 31  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-183-116-31

Query Match 83.3%; Score 1383; DB 9; Length 322;  
Best Local Similarity 83.5%; Pred. No. 5,8e-117;  
Matches 269; Conservative 16; Mismatches 37; Indels 0; Gaps 0;

QY 1 MDPRTSTDELTPTNGTEFTLCYQOTLSVLTIVTSVGLGTGNAVVLMLGCMRRNA 60  
DB 1 MDSITPVGTSLPTNGREETPCYKQTSIFGLTIVSLVLTGNAVVLMLGCMRRNA 60  
QY 61 FSIYILNLAADFLPLSGRLIYSLSFISPHITISKIIPVMMFESYFAGLSFLSAVSTER 120  
DB 61 VSIYILNVAADFLPLSGHIICSPRLINIKHPIISKIISPMTPTPYFGLMLSNISTER 120  
QY 121 CLSVAMPPIWRCHRPETHLSAVVLCVLLMALSLIRSLIEMMLCGFLFSGADSAMCOTSDPT 180  
DB 121 CLSIMPPIWRCHRPETHLSAVVLCVLLMALSLIRSLIEMMPCDFLFGADSVWCETSDPT 180  
QY 181 VAMIFPLCVVLCGSSVLVLRILIGSRKIPLTRIVYVTLVAVVLCGLFPGIOFTFL 240  
DB 181 IAMVFLCVVLCGSSVLVLRILIGSRKMPLTRIVYVTLVAVVLCGLFPGIOFTFL 240  
QY 241 WIHVDREVLFCVHVLVSIIFLSALNSSANPIIYFVFGSFRQRONRONTKLIVQALQDASE 300  
DB 241 RIHIDMKVLFCHVHLVSIIFLSALNSSANPIIYFVFGSFRQRONRONTKLIVQALQDPE 300  
QY 301 VDEGGGQLPEITLILSGSRLEQ 322  
DB 301 VDEGGGWLPEITLILSGSRLEQ 322

RESULT 5  
US-10-225-567A-674  
; Sequence 674, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: Lifespan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burner, Glenn C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A

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; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 674
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-674

Query Match      83.3%; Score 1383; DB 9; Length 322;
Best Local Similarity 83.5%; Pred. No. 5,8e-117;
Matches 269; Conservative 16; Mismatches 37; Indels 0; Gaps 0;

QY      1 MDPTSTLDTELPINGTGETTCYKQTLSLTVATCVSLVGLGNMVMMLLCGRMRNA 60
DB      1 MDSTIPVLGTETLPINGREETPCYKOTLSFTGTLCTVSALGNMVMMLLCGRMRNA 60
QY      61 FSIVILTAADPFLFSGRLIYSLSFSISIPHTISKILYPVMMSFYAGLSPLAVSTER 120
DB      61 VSIYLINVAADPFLFSGRHII CSPLRLINIRHPISKILSPVMFPPIFGSMISAISTER 120
QY      121 CLSVAMPPIWRCHRRPHLSAVVCVLLMALSLRSILEMMLCGLFSGADSAMCQTSDFIT 180
DB      121 CTSILMPPIWHRRRRPPYSVMCVLLMALSLRSILEMMFCCLFSGADSVMCESTDPIIT 180
QY      181 VAMLIFLCVVLGGSSLVLLIRILCGSRKIPLRLVYTILLTVVVFLLCGPFIQDPLFL 240
DB      181 IAMLVFLCVVLGGSSLVLLVRILCGSRKMPRLRYLTILLTVVVFLLCGPFIQDLIFS 240
QY      241 WIHVDREVLFCHVHLVSLFSLANSSANDPIYFVGSGFRONRONMKVLOPALODASE 300
DB      241 RHIDPMKVLFCHVHLVSLFSLANSSANDPIYFVGSGFRONRONMKVLOPALOPTPE 300
QY      301 VDGGGQLPEELIELSGSRLIQ 322
DB      301 VDGGGMPLPETIELSGSRLIQ 322

RESULT 6
US-10-219-834-79
; Sequence 79, Application US/10219834
; Publication No. US20030096751A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE THEREOF
FILE REFERENCE: D0191 NP
CURRENT APPLICATION NUMBER: US/10/219,834
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/313,658
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: US 60/340,703
PRIOR FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: US 60/318,675
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 60/355,596
PRIOR FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: US 60/333,417
PRIOR FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: US 60/338,367
PRIOR FILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn version 3.1
SEQ ID NO 79
LENGTH: 314
TYPE: PRT
ORGANISM: Homo sapiens
US-10-219-834-79

Query Match      80.3%; Score 1334; DB 9; Length 314;
Best Local Similarity 81.1%; Pred. No. 1.5e-112;
Matches 261; Conservative 16; Mismatches 37; Indels 8; Gaps 1;

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; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 674
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-674

Query Match      83.3%; Score 1383; DB 9; Length 322;
Best Local Similarity 83.5%; Pred. No. 5,8e-117;
Matches 269; Conservative 16; Mismatches 37; Indels 0; Gaps 0;

QY      1 MDPTSTLDTELPINGTGETTCYKQTLSLTVTCTIVSLVGLGNMVMMLLGRMRNA 60
DB      1 MDSTIPVLGTETLPINGREETPCYKOTLSFTGTLCTVSLALGNMVMMLLCGRMRNA 60
QY      61 FSIIYLTAADPFLFSGRLIYSLSFSISIPHTISKILYPVMMSFYAGLSPLAVSTER 120
DB      61 VSIYLIINVAADPFLFSGHIIICSPRLNIRHPISKILSPVMFPFPIGLSMIALSTER 120
QY      121 CLSVAMPITWRCHRPHTLSAVCVLLMALSLRSILEMMLCGLFSGADSAMCQTSFIT 180
DB      121 CTSILMPITWHRRRPRYSVMCVLLMALSLRSILEMMFCCLFGADSVWCETSDFIT 180
QY      181 VAMLIFLCVVLGGSSLVLRILICGSRKIPLRLYTYILLTVVVFLLCGPFIQPFLL 240
DB      181 IAMLVFLCVVLGGSSLVLRILICGSRKMPLRLRYTILLTVVVFLLCGPFIQQLIFS 240
QY      241 WIHVDREVLFCHVHLVSIFLSALNSANDPIYFVGSGFRONRONMKVLOPALODASE 300
DB      241 RHIDPMKVLFCHVHLVSIFLSALNSANDPIYFVGSGFRONRONMKVLOPALOPTPE 300
QY      301 VDGGGGLPEELIELSGSRLAQ 322
DB      301 VDGGGWLPEETIELSGSRLAQ 322

RESULT 6
US-10-219-834-79
; Sequence 79, Application US/10219834
; Publication No. US20030096751A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE THEREOF
FILE REFERENCE: D0191 NP
CURRENT APPLICATION NUMBER: US/10/219,834
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/313,658
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: US 60/340,703
PRIOR FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: US 60/318,675
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 60/355,596
PRIOR FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: US 60/333,417
PRIOR FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: US 60/338,367
PRIOR FILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn version 3.1
SEQ ID NO 79
LENGTH: 314
TYPE: PRT
ORGANISM: Homo sapiens
US-10-219-834-79

Query Match      80.3%; Score 1334; DB 9; Length 314;
Best Local Similarity 81.1%; Pred. No. 1.5e-112;
Matches 261; Conservative 16; Mismatches 37; Indels 8; Gaps 1;

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QY 1 MDPTISTLDTELPINGTEETLCYKOTLSLTVLTCIVSLVGLTGNAAVWMLLGCRRMNA 60
Db 1 MDSTIPVLGTELPINGREETPCYKOTLSFTGLTCIVSLVGLTGNAAVWMLLGCRRMNA 60
QY 61 FSIYIILMAAADFLFSGRLYSLSFISIPHTISKILYPVWMSYPAGLSFSAVSTER 120
Db 61 VSIYIILMAAADFLFSGRLYSLSFISIPHTISKILYPVWMSYPAGLSFSAVSTER 120
QY 121 CLSVLWPIWYRCRPHLSAVCVLWALSLRSILEMMLCGFLPSGADSWCOTSPFIT 180
Db 121 CLSVLWPIWYRCRPHLSAVCVLWALSLRSILEMMLCGFLPSGADSWCOTSPFIT 180
QY 181 VAMLIFFCVLVCSSVLVLRILCGSRKIPLTRLYVTILLTVLVFLCGLPFGIQLALY 240
Db 181 VAMLIFFCVLVCSSVLVLRILCGSRKIPLTRLYVTILLTVLVFLCGLPFGIQLALY 240
QY 241 WIHVDREVLFCVHLVSIPLSALNSSANPIYFFVGSFRORONMLKVLORALODASE 300
Db 241 RIHLDWVLFCHVHLVSIPLSALNSSANPIYFFVGSFRORONMLKVLORALODASE 300
QY 301 VDEGGQLPEETLELSSGRL 322
Db 293 VDEGGQLPEETLELSSGRL 314

RESULT 7
US-09-995-225-18
; Sequence 18, Application US/09995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huang T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Priddy, Cameron
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/1170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent version 3.1
; SEQ ID NO 18
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020193584A1el Sequence
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US-09-995-225-18
Query Match 77.9%; Score 1294; DB 9; Length 322;
Best Local Similarity 79.7%; Pred. No. 6.1e-109;
Matches 255; Conservative 20; Mismatches 45; Indels 0; Gaps 0;

QY 1 MDPTISTLDTELPINGTEETLCYKOTLSLTVLTCIVSLVGLTGNAAVWMLLGCRRMNA 60
Db 1 MDPTVPVFGTKLPLPINGREETPCYKOTLSFTGLTCIVSLVGLTGNAAVWMLLGCRRMNA 60
QY 61 FSIYIILMAAADFLFSGRLYSLSFISIPHTISKILYPVWMSYPAGLSFSAVSTER 120
Db 61 VSIYIILMAAADFLFSGRLYSLSFISIPHTISKILYPVWMSYPAGLSFSAVSTER 120
QY 121 CLSVLWPIWYRCRPHLSAVCVLWALSLRSILEMMLCGFLPSGADSWCOTSPFIT 180
Db 121 CLSVLWPIWYRCRPHLSAVCVLWALSLRSILEMMLCGFLPSGADSWCOTSPFIT 180
QY 181 VAMLIFFCVLVCSSVLVLRILCGSRKIPLTRLYVTILLTVLVFLCGLPFGIQLALY 240
Db 181 VAMLIFFCVLVCSSVLVLRILCGSRKIPLTRLYVTILLTVLVFLCGLPFGIQLALY 240
QY 241 WIHVDREVLFCVHLVSIPLSALNSSANPIYFFVGSFRORONMLKVLORALODASE 300
Db 241 RMHLDWVLFCHVHLVSIPLSALNSSANPIYFFVGSFRORONMLKVLORALODASE 300
QY 301 VDEGGQLPEETLELSSGRL 320
Db 301 VDEGGQLPEETLELSSGRL 320

RESULT 8
US-10-183-116-33
; Sequence 33, Application US/10183116
; Publication No. US2003092035A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
; APPLICANT: Dong, Xinzong
; APPLICANT: Zylka, Mark
; APPLICANT: Simon, Melvin
; APPLICANT: Han, Sang-Kyou
; TITLE OF INVENTION: PAIN SIGNALING MOLECULES
; FILE REFERENCE: CALTE.4C1CPI
; CURRENT APPLICATION NUMBER: US/10/183,116
; CURRENT FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/222,344
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: US 60/202,027
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 09/704,707
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/285,493
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/849,869
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-183-116-33

Query Match 77.9%; Score 1294; DB 9; Length 322;
Best Local Similarity 79.7%; Pred. No. 6.1e-109;
Matches 255; Conservative 20; Mismatches 45; Indels 0; Gaps 0;

QY 1 MDPTISTLDTELPINGTEETLCYKOTLSLTVLTCIVSLVGLTGNAAVWMLLGCRRMNA 60
Db 1 MDPTVPVFGTKLPLPINGREETPCYKOTLSFTGLTCIVSLVGLTGNAAVWMLLGCRRMNA 60
QY 61 FSIYIILMAAADFLFSGRLYSLSFISIPHTISKILYPVWMSYPAGLSFSAVSTER 120
Db 61 VSIYIILMAAADFLFSGRLYSLSFISIPHTISKILYPVWMSYPAGLSFSAVSTER 120
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Db 61 VSIYIINLAADFLFLSGRIIRSPRLINSHIRKILIVSVTPPTFGTSLMSAISTER 120  
Qy 121 CLSVLPMPWRCHRPHTLSAVVAVVLLWALSLRSLILEMMLCGFLFSGADSAMCOTSPFIT 180  
Db 121 CLSVLPMPWRCHRPHTLSAVVAVVLLWALSLRSLILEMMLCGFLFSGADSAMCOTSPFIT 180  
Qy 181 VAMILIFCVVLCVSVLIRILCGSRKIPRLRYVITLLTVLVPFLCGPFGIQLFPL 240  
Db 181 VAMILIFCVVLCVSVLIRILCGSRKIPRLRYVITLLTVLVPFLCGPFGIQLFPL 240  
Qy 241 WIHVREVLFCVHLVSIIFLSALNSSANPIIYFFVGSFRORONKLVQALQDASE 300  
Db 241 RMHLNLEVLCHVYLVCMSLSSANPIIYFFVGSFRORONKLVQALQDASE 300  
Qy 301 VDEGGQLPETILESGSRL 320  
Db 301 VDKGEGQLPERSLISGSRL 320

## RESULT 9

US-10-225-567a-689  
Sequence 689, Application US/10225567A  
Publication No. US20030113798A1  
GENERAL INFORMATION:  
APPLICANT: Lifespan Biosciences  
APPLICANT: Brown, Joseph P.  
APPLICANT: Burner, Glenn C.  
APPLICANT: Roush, Christine L.  
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
FILE REFERENCE: 1920-4-4  
CURRENT APPLICATION NUMBER: US/10/225,567A  
CURRENT FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/257,144  
PRIOR FILING DATE: 2000-12-19  
NUMBER OF SEQ ID NOS: 2292  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 689  
LENGTH: 322  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-225-567a-689

Query Match 77.9%; Score 1294; DB 9; Length 322;  
Best Local Similarity 79.7%; Pred. No. 6,1e-109;  
Matches 255; Conservative 20; Mismatches 45; Indels 0; Gaps 0;

Qy 1 MDPITSLDLELPINGTEETCYKQTLSTVLTCTIVSLVGLGNNAVVLMLGCRM RNA 60  
Db 1 MDPITSLDLELPINGTEETCYKQTLSTVLTCTIVSLVGLGNNAVVLMLGCRM RNA 60  
Qy 61 FSIYIINLAADFLFLSGRIIRSPRLINSHIRKILIVSVTPPTFGTSLMSAISTER 120  
Db 61 FSIYIINLAADFLFLSGRIIRSPRLINSHIRKILIVSVTPPTFGTSLMSAISTER 120  
Qy 121 CLSVLPMPWRCHRPHTLSAVVAVVLLWALSLRSLILEMMLCGFLFSGADSAMCOTSPFIT 180  
Db 121 CLSVLPMPWRCHRPHTLSAVVAVVLLWALSLRSLILEMMLCGFLFSGADSAMCOTSPFIT 180  
Qy 121 CLSVLPMPWRCHRPHTLSAVVAVVLLWALSLRSLILEMMLCGFLFSGADSAMCOTSPFIT 180  
Db 121 CLSVLPMPWRCHRPHTLSAVVAVVLLWALSLRSLILEMMLCGFLFSGADSAMCOTSPFIT 180  
Qy 181 VAMILIFCVVLCVSVLIRILCGSRKIPRLRYVITLLTVLVPFLCGPFGIQLFPL 240  
Db 181 VAMILIFCVVLCVSVLIRILCGSRKIPRLRYVITLLTVLVPFLCGPFGIQLFPL 240  
Qy 241 WIHVREVLFCVHLVSIIFLSALNSSANPIIYFFVGSFRORONKLVQALQDASE 300  
Db 241 RMHLNLEVLCHVYLVCMSLSSANPIIYFFVGSFRORONKLVQALQDASE 300  
Qy 301 VDEGGQLPETILESGSRL 320  
Db 301 VDKGEGQLPERSLISGSRL 320

RESULT 10  
US-10-219-834-20

Sequence 20, Application US/10219834  
Publication No. US20030096751A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE THEREIN  
FILE REFERENCE: D0191 NP  
CURRENT APPLICATION NUMBER: US/10/219,834  
CURRENT FILING DATE: 2002-08-15  
PRIOR APPLICATION NUMBER: US 60/313,658  
PRIOR FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: US 60/340,703  
PRIOR FILING DATE: 2001-10-30  
PRIOR APPLICATION NUMBER: US 60/318,675  
PRIOR FILING DATE: 2001-09-12  
PRIOR APPLICATION NUMBER: US 60/355,596  
PRIOR FILING DATE: 2002-02-06  
PRIOR APPLICATION NUMBER: US 60/333,417  
PRIOR FILING DATE: 2001-11-26  
PRIOR APPLICATION NUMBER: US 60/338,367  
PRIOR FILING DATE: 2001-12-06  
NUMBER OF SEQ ID NOS: 192  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 20  
LENGTH: 328  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-219-834-20

Query Match 73.0%; Score 1212; DB 9; Length 328;  
Best Local Similarity 74.7%; Pred. No. 1.6e-101;  
Matches 245; Conservative 17; Mismatches 60; Indels 6; Gaps 2;

Qy 1 MDPITSLDLELPINGTEETCYKQTLSTVLTCTIVSLVGLGNNAVVLMLGCRM RNA 60  
Db 1 MDPITSLDLELPINGTEETCYKQTLSTVLTCTIVSLVGLGNNAVVLMLGCRM RNA 60  
Qy 61 FSIYIINLAADFLFLSGRIIRSPRLINSHIRKILIVSVTPPTFGTSLMSAISTER 120  
Db 61 FSIYIINLAADFLFLSGRIIRSPRLINSHIRKILIVSVTPPTFGTSLMSAISTER 120  
Qy 117 STERCLSVLPMPWRCHRPHTLSAVVAVVLLWALSLRSLILEMMLCGFLFSGADSAMCOTS 176  
Db 117 STERCLSVLPMPWRCHRPHTLSAVVAVVLLWALSLRSLILEMMLCGFLFSGADSAMCOTS 176  
Qy 121 STERCLSVLPMPWRCHRPHTLSAVVAVVLLWALSLRSLILEMMLCGFLFSGADSAMCOTS 180  
Db 121 STERCLSVLPMPWRCHRPHTLSAVVAVVLLWALSLRSLILEMMLCGFLFSGADSAMCOTS 180  
Qy 177 DFTVAMLIFLCVGLGSSVLLIRILCGSRKIPRLRYVITLLTVLVPFLCGPFGIQLFPL 240  
Db 177 DFTVAMLIFLCVGLGSSVLLIRILCGSRKIPRLRYVITLLTVLVPFLCGPFGIQLFPL 240  
Qy 237 FLEWIVHREVLFCVHLVSIIFLSALNSSANPIIYFFVGSFRORONKLVQALQDASE 294  
Db 237 FLEWIVHREVLFCVHLVSIIFLSALNSSANPIIYFFVGSFRORONKLVQALQDASE 294  
Qy 241 FLLIMVKSVDVLFCHHPVSVLSSANPIIYFFVGSFRORONKLVQALQDASE 300  
Db 241 FLLIMVKSVDVLFCHHPVSVLSSANPIIYFFVGSFRORONKLVQALQDASE 300  
Qy 295 LODASEVDEGGQLPETILESGSRL 322  
Db 295 LODASEVDEGGQLPETILESGSRL 322

## RESULT 11

US-10-183-116-18  
Sequence 18, Application US/10183116  
Publication No. US20030092035A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, David J.  
APPLICANT: Dong, Xinzhang  
APPLICANT: Zyika, Mark  
APPLICANT: Simon, Melvin  
APPLICANT: Han, Sang-kyou  
TITLE OF INVENTION: PAIN SIGNALING MOLECULES  
FILE REFERENCE: CALTE, 4C1CPI  
CURRENT APPLICATION NUMBER: US/10/183,116  
CURRENT FILING DATE: 2002-06-26  
PRIOR APPLICATION NUMBER: US 60/222,344  
PRIOR FILING DATE: 2000-08-01

PRIOR APPLICATION NUMBER: US 60/202,027  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: US 09/704,707  
PRIOR FILING DATE: 2000-11-03  
PRIOR APPLICATION NUMBER: US 60/285,493  
PRIOR FILING DATE: 2001-04-19  
PRIOR APPLICATION NUMBER: US 09/849,869  
PRIOR FILING DATE: 2001-05-04  
NUMBER OF SEQ ID NOS: 109  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 18  
LENGTH: 330  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-183-116-18

Query Match 62.5%; Score 1038.5; DB 9; Length 330;  
Best Local Similarity 64.7%; Pred. No. 7e-86;  
Matches 213; Conservative 27; Mismatches 80; Indels 9; Gaps 3;

QY 1 MDPTISTDTELTPTNGTEET---LCYKQTLSTLVTCIVSLVGLTGNAAVLMILGCMR 57  
DB 1 MDPTTPAMGTESTTVNGDQALLLCKGKETLIPVFLIFIALVGLVNGFVLMILGFRMR 60  
QY 58 RNAFSIYILNLAADFLFLSGRLIYSLT---SFISIPHTISKILYPMWMSYFAGLSFL 113  
DB 61 RNAFSVYVLSLAGDFLFLCQIINCIVLYSNFPCISINFPSTFTVMCAVLAGLSML 120  
QY 114 SAVSTERCLSVLWPIWRCRPHTHLSAVCVLMAALSILRSILEMMLCGFLPSGADSAWC 173  
DB 121 STVSTERCLSVLWPIWRCRPRHLSAVCVLMAALSILRSILEMMLCGFLPSGDSGWC 180  
QY 174 QTSDFITVAMLIPLFCVVLGSSSLVLRILIGSRKIPLTRLYVTITLVVFLICGLPFG 233  
DB 181 QTFPFTITAMLIPLFMVLGSSSLALVRLILGSRKLPTRLYVTITLVVFLICGLPFG 240  
QY 234 IQFPLFIWHDREVLFCHVHLVSIPLSALNSSANPIIYFVSGFRORONR--LKLVL 291  
DB 241 IQWFLIIMKDSVLFCHIHVPSVVLSSINSSANPIIYFVSGFRKQWRLQOPILKAL 300  
QY 292 QRALODASEVDEGGGQLPEBILLSGRL 320  
DB 301 QRALODIAEVDHSEGCRCGTPEMSRSSL 329

RESULT 12  
US-10-079-384-12  
Sequence 12, Application US/10079384  
Publication No. US20030108986A1  
GENERAL INFORMATION:  
APPLICANT: Communi, Didier  
TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS  
FILE REFERENCE: 9409/2132  
CURRENT APPLICATION NUMBER: US/10/079,384  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 09/885,453  
PRIOR FILING DATE: 2001-06-20  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 12  
LENGTH: 330  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-079-384-12

Query Match 62.5%; Score 1038.5; DB 9; Length 330;  
Best Local Similarity 64.7%; Pred. No. 7e-86;  
Matches 213; Conservative 27; Mismatches 80; Indels 9; Gaps 3;  
QY 1 MDPTISTDTELTPTNGTEET---LCYKQTLSTLVTCIVSLVGLTGNAAVLMILGCMR 57  
DB 1 MDPTTPAMGTESTTVNGDQALLLCKGKETLIPVFLIFIALVGLVNGFVLMILGFRMR 60

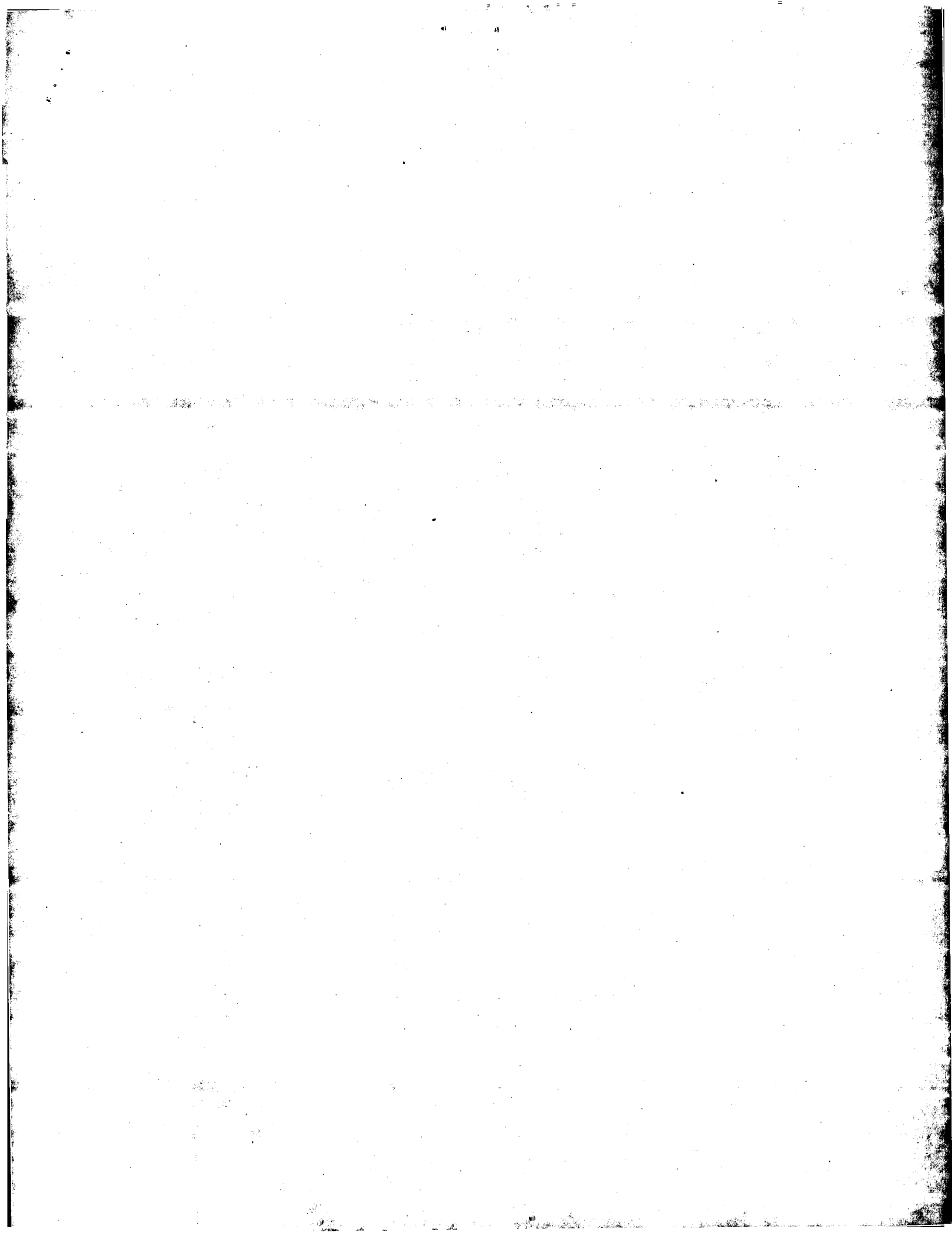
QY 58 RNAFSIYILNLAADFLFLSGRLIYSLT---SFISIPHTISKILYPMWMSYFAGLSFL 113  
DB 61 RNAFSVYVLSLAGDFLFLCQIINCIVLYSNFPCISINFPSTFTVMCAVLAGLSML 120  
QY 114 SAVSTERCLSVLWPIWRCRPHTHLSAVCVLMAALSILRSILEMMLCGFLPSGADSAWC 173  
DB 121 STVSTERCLSVLWPIWRCRPRHLSAVCVLMAALSILRSILEMMLCGFLPSGDSGWC 180  
QY 174 QTSDFITVAMLIPLFCVVLGSSSLVLRILIGSRKIPLTRLYVTITLVVFLICGLPFG 233  
DB 181 QTFPFTITAMLIPLFMVLGSSSLALVRLILGSRKLPTRLYVTITLVVFLICGLPFG 240  
QY 234 IQFPLFIWHDREVLFCHVHLVSIPLSALNSSANPIIYFVSGFRORONR--LKLVL 291  
DB 241 IQWFLIIMKDSVLFCHIHVPSVVLSSINSSANPIIYFVSGFRKQWRLQOPILKAL 300  
QY 292 QRALODASEVDEGGGQLPEBILLSGRL 320  
DB 301 QRALODIAEVDHSEGCRCGTPEMSRSSL 329

RESULT 13  
US-10-225-567A-649  
Sequence 649, Application US/10225567A  
Publication No. US20030113798A1  
GENERAL INFORMATION:  
APPLICANT: Lifespan BioSciences  
APPLICANT: Brown, Joseph P.  
APPLICANT: Burnet, Glenna C.  
APPLICANT: Roush, Christine L.  
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
FILE REFERENCE: 1920-4-4  
CURRENT APPLICATION NUMBER: US/10/225,567A  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/257,144  
PRIOR FILING DATE: 2000-12-19  
NUMBER OF SEQ ID NOS: 2292  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 649  
LENGTH: 330  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-225-567A-649

Query Match 62.5%; Score 1038.5; DB 9; Length 330;  
Best Local Similarity 64.7%; Pred. No. 7e-86;  
Matches 213; Conservative 27; Mismatches 80; Indels 9; Gaps 3;

QY 1 MDPTISTDTELTPTNGTEET---LCYKQTLSTLVTCIVSLVGLTGNAAVLMILGCMR 57  
DB 1 MDPTTPAMGTESTTVNGDQALLLCKGKETLIPVFLIFIALVGLVNGFVLMILGFRMR 60  
QY 58 RNAFSIYILNLAADFLFLSGRLIYSLT---SFISIPHTISKILYPMWMSYFAGLSFL 113  
DB 61 RNAFSVYVLSLAGDFLFLCQIINCIVLYSNFPCISINFPSTFTVMCAVLAGLSML 120  
QY 114 SAVSTERCLSVLWPIWRCRPHTHLSAVCVLMAALSILRSILEMMLCGFLPSGADSAWC 173  
DB 121 STVSTERCLSVLWPIWRCRPRHLSAVCVLMAALSILRSILEMMLCGFLPSGDSGWC 180  
QY 174 QTSDFITVAMLIPLFCVVLGSSSLVLRILIGSRKIPLTRLYVTITLVVFLICGLPFG 233  
DB 181 QTFPFTITAMLIPLFMVLGSSSLALVRLILGSRKLPTRLYVTITLVVFLICGLPFG 240  
QY 234 IQFPLFIWHDREVLFCHVHLVSIPLSALNSSANPIIYFVSGFRORONR--LKLVL 291  
DB 241 IQWFLIIMKDSVLFCHIHVPSVVLSSINSSANPIIYFVSGFRKQWRLQOPILKAL 300  
QY 292 QRALODASEVDEGGGQLPEBILLSGRL 320  
DB 301 QRALODIAEVDHSEGCRCGTPEMSRSSL 329







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## OM protein - protein search, using sw model

Run on: July 2, 2003, 19:19:30 ; Search time 14 Seconds  
(without alignments)  
676.727 Million cell updates/sec

Title: US-09-849-869A-16

Perfect score: 1661  
Sequence: 1 MDPSTLDELTPINGTE.....EGGGQLPEELLSGRLEQ 322Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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- 2: /cgn2\_6/ptodata/1/1aa/5B COMB pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A COMB pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B COMB pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PTUS COMB pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfile1.pcp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	451.5	27.2	325	5320941-2	Patent No. 5320941
2	410.5	24.7	282	US-08-118-270-52	Sequence 52, Appl
3	410.5	24.7	282	PCT-US93-08528-52	Sequence 52, Appl
4	384	23.1	298	US-08-118-270-76	Sequence 76, Appl
5	384	23.1	298	PCT-US93-08528-76	Sequence 76, Appl
6	279.5	16.8	395	US-08-981-825-6	Sequence 6, Appl
7	279.5	16.8	395	US-08-981-825-6	Sequence 6, Appl
8	250	15.1	350	US-08-480-784-6	Sequence 6, Appl
9	243.5	14.7	369	US-08-480-784-6	Sequence 6, Appl
10	243.5	14.7	369	US-08-480-784-6	Sequence 6, Appl
11	243.5	14.7	369	US-08-480-784-6	Sequence 6, Appl
12	241.5	14.5	369	US-08-480-784-6	Sequence 6, Appl
13	241.5	14.5	369	US-08-480-784-6	Sequence 6, Appl
14	241.5	14.5	369	US-08-480-784-6	Sequence 6, Appl
15	236	14.2	364	US-08-120-601B-9	Sequence 9, Appl
16	226	13.6	354	US-07-759-568-2	Sequence 2, Appl
17	224	13.5	381	US-08-467-125-2	Sequence 2, Appl
18	224	13.5	381	US-08-467-125-2	Sequence 2, Appl
19	224	13.5	381	US-08-911-320A-2	Sequence 2, Appl
20	222	13.4	380	US-08-217-101-2	Sequence 2, Appl
21	219.5	13.2	369	US-08-676-351-5	Sequence 5, Appl
22	219.5	13.2	369	US-07-816-283-6	Sequence 6, Appl
23	219.5	13.2	369	US-08-417-103-6	Sequence 6, Appl
24	219.5	13.2	369	US-08-417-103-6	Sequence 6, Appl
25	219	13.2	304	US-09-071-434-3	Sequence 3, Appl
26	219	13.2	304	US-08-118-270-35	Sequence 35, Appl
27	218.5	13.2	333	PCT-US93-08528-35	Sequence 35, Appl
				US-08-148-215A-4	Sequence 4, Appl

28	218.5	13.2	391	4	US-08-120-601B-8	Sequence 8, Appl
29	218	13.1	380	1	US-08-149-093A-7	Sequence 7, Appl
30	218	13.1	380	2	US-08-911-245-7	Sequence 7, Appl
31	218	13.1	380	4	US-08-188-275A-5	Sequence 5, Appl
32	218	13.1	380	4	US-09-510-473-7	Sequence 7, Appl
33	218	13.1	380	4	US-09-351-198-5	Sequence 5, Appl
34	218	13.1	380	4	US-09-113-426-5	Sequence 5, Appl
35	217.5	13.1	350	1	US-07-759-568-3	Sequence 3, Appl
36	217	13.1	259	4	US-09-261-599B-3	Sequence 3, Appl
37	217	13.1	259	4	US-09-456-455A-3	Sequence 3, Appl
38	217	13.1	380	3	US-08-147-592A-2	Sequence 2, Appl
39	217	13.1	380	4	US-08-292-694A-2	Sequence 2, Appl
40	215	12.9	428	1	US-07-816-283-12	Sequence 12, Appl
41	215	12.9	428	1	US-08-417-103-12	Sequence 12, Appl
42	214	12.9	394	4	US-08-405-271A-22	Sequence 22, Appl
43	213	12.8	370	3	US-08-781-250-2	Sequence 2, Appl
44	212.5	12.8	315	1	US-08-118-270-34	Sequence 34, Appl
45	212.5	12.8	315	5	PCT-US93-08528-34	Sequence 34, Appl

## ALIGNMENTS

RESULT 1  
5320941-2  
Patent No. 5320941  
APPLICANT: Young, Dallan, Wigler, Michael H., Fasano  
; Octavio  
; TITLE OF INVENTION: DNA SEQUENCES ENCODING MAS ONHCOGENE,  
; POLYPEPTIDES ENCODED THEREFROM AND DIAGNOSTIC AND OTHER METHODS  
; BASED THEREFROM  
; NUMBER OF SEQUENCES: 2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/06/872,087  
; FILING DATE: 06-JUN-1986  
; SEQ ID NO: 2:  
; LENGTH: 325  
5320941-2

Query Match 27.2%; Score 451.5; DB 6; length 325;  
Best Local Similarity 38.4%; Pred. No. 3.4e-29;  
Matches 103; Conservative 59; Mismatches 95; Indels 11; Gaps 4;

QY	37	VSIVGLTGNVYVWLGCRMRRAFSITVILNLAADFLPSGLI----	YLSIFSIPH 92
DB	42	ISPVGVEVNGILMPFCFRRRNPFTVYTHSIAISILFCIFILSIDALDYELSSGH 101	
QY	93	TISKILYPV-MMFSYFAGLSFLSAVSTERCISVLMPIWYRCHPRLSAVAVCVLMAVSL 151	
DB	102	YTVIVLSTVFLFGVYTGILYLAISVERCLSTVYIWRCHRPKQXALVCAVLAALASC 161	
QY	152	LRLSEFMMLCGFLPSGADSNACQTSDFITVAMILFCV--VLCGSSLVILIRILGSRKI 209	
DB	162	LVTVMYVNCVCHTEESDSBPNDCAVIFPAISFLVFGMLVSSITLVKIPKXTWAS 221	
QY	210	PLRLVTVLTLVTLVGLSPGICQFLFMVHVRVLFCHVHVSIFLSLNSANP 269	
DB	222	HSSKLIVLVWITLITFLI-----FAMKRLLYLVYEWSTFGNHLDISLFLSTINSANN 277	
QY	270	IIVFVSGFRORONRONTKLVLORALOD 297	
DB	278	FIFVFGSSKKRKFQSLKVTTRAFKD 305	
RESULT 2			
US-08-118-270-52			
; Sequence 52, Application US/08118270			
; Patent No. 5508384			
; GENERAL INFORMATION:			
; APPLICANT: Murphy, Randall B.			
; APPLICANT: Schuster, David I.			
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN			
; RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF			

NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/118,270  
FILING DATE: 09-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY=2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 282 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-118-270-52

Query Match 24.7%; Score 410.5; DB 1; Length 282;  
Best Local Similarity 37.2%; Pred. No. 5.8e-26;  
Matches 100; Conservative 58; Mismatches 88; Indels 23; Gaps 9;

QY 37 VSLVGLTGNVAVMLGCRMRNNAFSIYI-LNLAADFLF---LSGRLLYSLSISIP 91  
DB 9 ISPGFVENGILLWFL-C-----FFVYTHLSIADISLFCIFILS-IDYALDYELSSG 60  
QY HTISKILLYPV-MMSYFAGLSFSAVSTERCISVMPWIRCHRPHTLSAVVCYLWALS 150  
DB 61 HYIIVTLSTVFLFGYNTGLYLLTAISVERCLSVYPIWYCHRPKYQSAVLCALLWALS 120  
QY 151 LRSILEMMLCGFLFSGADSAMCQTSDFITVAMLIFFCVLGCSSVLVLLIRILGSRKIP 210  
DB 121 CLVVTM-YVNCIDRFESHSHNDRAVITFIALISFLVFTPSVSTLIVKIRKNTWASH 179  
QY 211 LTRLVYTLTLVAVFLLCGLPFGIOFLF--LMIHDEVLFCHVHLVSIFLSALNSAN 268  
DB 180 SSKRYIVIMVTIIFLIFFAMPRLVLYLYEYW-----STFGNLHHSILSFSTINSAN 233  
QY 269 PIIFYFVGSFRORONKLVLOALOD 297  
DB 234 PFIIFYVSSSKKRKESLKVVLTRAFKD 262

RESULT 3  
PCT-US93-08528-52  
Sequence 52, Application PC/TUS9308528  
GENERAL INFORMATION:  
APPLICANT: New York University  
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington

STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: PCT/US93/08528  
FILING DATE: 09-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 282 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-08528-52

Query Match 24.7%; Score 410.5; DB 5; Length 282;  
Best Local Similarity 37.2%; Pred. No. 5.8e-26;  
Matches 100; Conservative 58; Mismatches 88; Indels 23; Gaps 9;

QY 37 VSLVGLTGNVAVMLGCRMRNNAFSIYI-LNLAADFLF---LSGRLLYSLSISIP 91  
DB 9 ISPGFVENGILLWFL-C-----FFVYTHLSIADISLFCIFILS-IDYALDYELSSG 60  
QY HTISKILLYPV-MMSYFAGLSFSAVSTERCISVMPWIRCHRPHTLSAVVCYLWALS 150  
DB 61 HYIIVTLSTVFLFGYNTGLYLLTAISVERCLSVYPIWYCHRPKYQSAVLCALLWALS 120  
QY 151 LRSILEMMLCGFLFSGADSAMCQTSDFITVAMLIFFCVLGCSSVLVLLIRILGSRKIP 210  
DB 121 CLVVTM-YVNCIDRFESHSHNDRAVITFIALISFLVFTPSVSTLIVKIRKNTWASH 179  
QY 211 LTRLVYTLTLVAVFLLCGLPFGIOFLF--LMIHDEVLFCHVHLVSIFLSALNSAN 268  
DB 180 SSKRYIVIMVTIIFLIFFAMPRLVLYLYEYW-----STFGNLHHSILSFSTINSAN 233  
QY 269 PIIFYFVGSFRORONKLVLOALOD 297  
DB 234 PFIIFYVSSSKKRKESLKVVLTRAFKD 262

RESULT 4  
US-08-118-270-76  
Sequence 76, Application US/08118270  
GENERAL INFORMATION:  
APPLICANT: Murphy, Randall B.  
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/118,270  
FILING DATE: 09-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY-2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 298 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-118-270-76

Query Match 23.1%; Score 384; DB 1; Length 298;  
Best Local Similarity 32.7%; Pred. No. 8,4e-24;  
Matches 97; Conservative 60; Mismatches 102; Indels 38; Gaps 11;

QY 36 IVSLVGLTGNVAVMLGCRMRNAPSIIYI-LNLAAADFLISGRLLYSLL---SFI-S 89  
DB 8 LLLCGLVNGLVNGLVWFGFSIKRTPSIYIFLHIASADGILYFSKAVIALNLNGTFLGS 67  
QY 90 IPTHISKLIVPMVMSYFAGLSFLSAVSTERCLSVLMPWYRCHRPHTLSAVVCVLLMAL 149  
DB 68 FPDYVRV-SRIVGLTFPAGVSLPALSIERCVSIFPMWYRRPRKSLAGVALLML 126  
QY 150 SLRSLIEMMLCGFLFSGADSAWQTSDFITVAMLIF---LCVVLGSSVLLIRILC 204  
DB 127 SFLVTSIHNVFC-LHGHSAGTACLNMDISLIGILFELFCPIWVLC---IALHVEC 181  
QY 205 GSRKIPLT-RLVYITLITVFLVLLCGLPFGIOFLELWI-----HDEVLFCHVHL 255  
DB 182 RARRRQSAKLNHVLAIVSVFLVSSITLIGIDWFLF-WFQIPAPPEPVYRDLCIC--- 236  
QY 256 VSIFLSALNSSANPIYFVGSFRORONRQNLKVLQALODASEVDEGGQOLPEEI 312  
DB 237 -----INSSAKPIVFIAGRDKSQRLMEPLRVVFORALRDGABPDGAASSTPTNV 286

RESULT 5:  
PCT-US93-08528-76  
Sequence 76, Application PC/TUS9308528  
GENERAL INFORMATION:  
APPLICANT: New York University  
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08528  
FILING DATE: 09-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 298 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-08528-76

Query Match 23.1%; Score 384; DB 5; Length 298;  
Best Local Similarity 32.7%; Pred. No. 8,4e-24;  
Matches 97; Conservative 60; Mismatches 102; Indels 38; Gaps 11;

QY 36 IVSLVGLTGNVAVMLGCRMRNAPSIIYI-LNLAAADFLISGRLLYSLL---SFI-S 89  
DB 8 LLLCGLVNGLVNGLVWFGFSIKRTPSIYIFLHIASADGILYFSKAVIALNLNGTFLGS 67  
QY 90 IPTHISKLIVPMVMSYFAGLSFLSAVSTERCLSVLMPWYRCHRPHTLSAVVCVLLMAL 149  
DB 68 FPDYVRV-SRIVGLTFPAGVSLPALSIERCVSIFPMWYRRPRKSLAGVALLML 126  
QY 150 SLRSLIEMMLCGFLFSGADSAWQTSDFITVAMLIF---LCVVLGSSVLLIRILC 204  
DB 127 SFLVTSIHNVFC-LHGHSAGTACLNMDISLIGILFELFCPIWVLC---IALHVEC 181  
QY 205 GSRKIPLT-RLVYITLITVFLVLLCGLPFGIOFLELWI-----HDEVLFCHVHL 255  
DB 182 RARRRQSAKLNHVLAIVSVFLVSSITLIGIDWFLF-WFQIPAPPEPVYRDLCIC--- 236  
QY 256 VSIFLSALNSSANPIYFVGSFRORONRQNLKVLQALODASEVDEGGQOLPEEI 312  
DB 237 -----INSSAKPIVFIAGRDKSQRLMEPLRVVFORALRDGABPDGAASSTPTNV 286

RESULT 6:  
US-08-981-825-6  
Sequence 6, Application US/08981825  
Patent No. 6040426  
GENERAL INFORMATION:  
APPLICANT: OGAWA, KAZUYAUKI  
APPLICANT: TANAKA, KAZUYA  
APPLICANT: NAGATA, KINYA  
APPLICANT: TAKANO, SYOICHI  
TITLE OF INVENTION: PROTEIN SPECIFIC TO HUMAN  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM COMPATIBLE  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:



COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458, 970A  
FILING DATE: June 2, 1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/09234  
FILING DATE: 16 AUG 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: MULLINS, J.G.  
REGISTRATION NUMBER: 33,073  
REFERENCE/DOCKET NUMBER: 325800-353  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 350 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-458-970A-9

Query Match 15.1%; Score 250; DB 2; Length 350;  
Best Local Similarity 26.6%; Pred. No. 6,1e-13;  
Matches 89; Conservative 56; Mismatches 130; Indels 60; Gaps 10;

QY 7 TLDLDELPIINTEETELCYKQTLSTLVLTCTISLVGLTGNNAVLM-LIGCRMRAFSYIL 66  
DB 19 TLDLN-TPVDTSNLTVPDIL-VLPVAVLVGLNNAVVTAEARRTNALWFL 76  
QY 67 NLAADFL-FLSGRLIYSLFSISIPH-----TISKILYPMWMSYFAGLSFLSAVSTER 120  
DB 77 NLAADFLSGRLIYSLFSISIPH-----TISKILYPMWMSYFAGLSFLSAVSTER 134  
QY 121 CLSLVLMPIWCHRPHTLSAVVAVVLMALSLRSILEMMLCGFLPSGADSAMCOTSDPIT 180  
DB 135 FLVFKPIWCFNFGAGLAWIACAVAMGLALLITPSFL-----YRV 176  
QY 181 VAMLIPLCVLVC-----SSLVLTIRILGCS-RKIPLTFLVYTIIL----- 220  
DB 177 VREYFPKVLGCVDYSHDKRERAVAIYRLVGLFPLTLTTCYFILTIRTSRATR 236  
QY 221 -----TVLVFLLCGLPFGIQLFLMIHVDRVLFCHVLSIFLS--ALNSAN 268  
DB 237 STKLKVVAVVAVASFIFWLPYQVTGIMMSFLPSSPTFLINKLDSLCVSFAVINCIN 296  
QY 269 PIIFYFVGSFRORONRLKIVLQALODASEVD 303  
DB 297 PIIVVAGQGFQGRKLSPLSLRNVLTEESVRE 331

## RESULT 9

US-08-411-859-3  
Sequence 3, Application US/08411859  
Patent No. 5985600  
GENERAL INFORMATION:  
APPLICANT: EVANS, CHRISTOPHER J.  
APPLICANT: KEITH JR., DUANE E.  
APPLICANT: EDWARDS, ROBERT H.  
TITLE OF INVENTION: EXPRESSION CLONING OF A DELTA OPIOID  
TITLE OF INVENTION: RECEPTOR RELATED EXPRESSION SYSTEMS, AND RELATED  
TITLE OF INVENTION: PHARMACEUTICALS  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto

STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/411, 859  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/929, 200  
FILING DATE: 13-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: LITHGOW, TIMOTHY J.  
REGISTRATION NUMBER: 36,856  
REFERENCE/DOCKET NUMBER: 22000-20526.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-813-5600  
TELEFAX: 415-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 369 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-411-859-3

Query Match 14.7%; Score 243.5; DB 2; Length 369;  
Best Local Similarity 27.6%; Pred. No. 2.2e-12;  
Matches 96; Conservative 57; Mismatches 126; Indels 69; Gaps 13;

QY 3 PTISTLDTELPINGTEETELCYKQTLSTLVLTCTISLVGLTGNNAVLM-LIGCRMRR 58  
DB 16 PSPFDLNGSLPENGNSNGTEPYDMTSMNVLTITIVVVCVGLCGNTIVYILRAKMK 75  
QY 59 NAFSIYILNLAADFL-FLSGRLIYSLFSISIPH-----TISKILYPMWMSYFAGLSFL 113  
DB 76 TITNIYILNLAIDELFMGL--LPFLAMQVALVHWPFKAIQVMTVDSINOFTSIFCL 133  
QY 114 SAVTERCISLVMPWCHRPHTLSAVVAVVLMALSLRSILEMML----- 160  
DB 134 TWSIDRYLVAVPIISAKRRPRITAKINWAVGSLV-VLPIMIVAGLRNONGRSS 192  
QY 161 CGFLPSGADSAMCOTSDPITVAMLIPLCV-----VLGSSVLTLIR-----ILGSRKIPLT 212  
DB 193 CTINWPGESGAW--YGFITVAVILGLVPLTITICYLEFIIIKVSSGIRVGSSRKKS 250  
QY 213 RLVT--ILTLVAVFLLCGLPFGIQLFLMIHVDRVLFCHVLS----- 257  
DB 251 EKVTRWVSIVAVVFLFCWLP---FYIF-----NVSVSVALSPPALKGMF 294  
QY 258 ---IFLSALNSANPIIFYFVGSFRORONRLKIVLQALODASEVD 302  
DB 295 DPAVILTYANSCANPIIYAFSLDNFKKSFQNVLCIVKVGAEDEGRSD 342

## RESULT 10

US-08-387-707-9  
Sequence 9, Application US/08387707  
Patent No. 625563  
GENERAL INFORMATION:  
APPLICANT: EVANS, CHRISTOPHER J.  
APPLICANT: KEITH, DUANE E.  
TITLE OF INVENTION: OPIOID RECEPTOR GENES  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, N.W. Suite 5500  
CITY: Washington

STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/387,707  
FILING DATE: 10-SEP-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: MORASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22000-20526.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 369 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-387-707-9

Query Match 14.7%; Score 243.5; DB 4; Length 369;  
Best Local Similarity 27.6%; Pred. No. 2.2e-12;  
Matches 96; Conservative 57; Mismatches 126; Indels 69; Gaps 13;

QY 3 PTSTLDELTPINGTEETLCYKQTLSTLVLCI---VSLNGLTGNAAVLW-LLGCRMR 58  
DB 16 PSPFDLNGSLGNSNGQTEPYDMTSNAVLFTFYVVCVGLCGTLVTVILRYAKK 75  
QY 59 NAFSIYIUNLAADFLSLGRILYSLFSISPH-----TISKILYPMWMSYFAGLSFL 113  
DB 76 TITNIYIUNLADELFLMG--LPFLAQVALVHMPFGKALCRVMTVDGINQFISICL 133  
QY 114 SAVSTERCLSVLPWYRCHPRTL SAVVCVLLMALSLRSLIEMWL----- 160  
DB 134 TWMSIDRYLAIVHPILKAKRRPRTAKMINVAVGVSLL-VILPIMIYAGLRNQGRRS 192  
QY 161 CGFLPSGADSAWCSQSDFTVAMLFCLV---VLGSSVLVLR-----ILGSRKIPLT 212  
DB 193 CTINMPGSGAW--YTGFIYAFILGFLVPLTITICLCTYFTIKVSSGIRVSSRRKKS 250  
QY 213 RLVT--ILTVLVFLLCGLPFGIOFELFLMIVHREVLFCVHLVS----- 257  
DB 251 EKVTRMWSIVAVFICWLP---FYIF-----NVSSVSAISPTPAKGMF 294  
QY 258 ---IFLSALNSSANPIIYFVGSFRORONRUKLVQLRALODASEVD 302  
DB 295 DFVILITVANSANPIIYAFILSDNFKKSFQNVLCVKGSGADGERSD 342

RESULT 11  
US-08-405-271A-9  
Sequence 9, Application US/08405271A  
Patent No. 6432652  
GENERAL INFORMATION:  
APPLICANT: EVANS, CHRISTOPHER J.  
TITLE OF INVENTION: OPIOID RECEPTOR GENES  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/405,271A  
FILING DATE: 14-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MORASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22000-20526.22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 369 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-405-271A-9

Query Match 14.7%; Score 243.5; DB 4; Length 369;  
Best Local Similarity 27.6%; Pred. No. 2.2e-12;  
Matches 96; Conservative 57; Mismatches 126; Indels 69; Gaps 13;

QY 3 PTSTLDELTPINGTEETLCYKQTLSTLVLCI---VSLNGLTGNAAVLW-LLGCRMR 58  
DB 16 PSPFDLNGSLGNSNGQTEPYDMTSNAVLFTFYVVCVGLCGTLVTVILRYAKK 75  
QY 59 NAFSIYIUNLAADFLSLGRILYSLFSISPH-----TISKILYPMWMSYFAGLSFL 113  
DB 76 TITNIYIUNLADELFLMG--LPFLAQVALVHMPFGKALCRVMTVDGINQFISICL 133  
QY 114 SAVSTERCLSVLPWYRCHPRTL SAVVCVLLMALSLRSLIEMWL----- 160  
DB 134 TWMSIDRYLAIVHPILKAKRRPRTAKMINVAVGVSLL-VILPIMIYAGLRNQGRRS 192  
QY 161 CGFLPSGADSAWCSQSDFTVAMLFCLV---VLGSSVLVLR-----ILGSRKIPLT 212  
DB 193 CTINMPGSGAW--YTGFIYAFILGFLVPLTITICLCTYFTIKVSSGIRVSSRRKKS 250  
QY 213 RLVT--ILTVLVFLLCGLPFGIOFELFLMIVHREVLFCVHLVS----- 257  
DB 251 EKVTRMWSIVAVFICWLP---FYIF-----NVSSVSAISPTPAKGMF 294  
QY 258 ---IFLSALNSSANPIIYFVGSFRORONRUKLVQLRALODASEVD 302  
DB 295 DFVILITVANSANPIIYAFILSDNFKKSFQNVLCVKGSGADGERSD 342

RESULT 12  
US-07-816-283-8  
Sequence 8, Application US/07816283  
Patent No. 5436155  
GENERAL INFORMATION:  
APPLICANT: Bell, Graeme I.  
APPLICANT: Yamada, Yutichiro  
APPLICANT: Seino, Susumu  
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: PO Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible



CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Wilson, Mark B.  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOCKET NUMBER: INDA.002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 369 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-120-601B-9

Query Match 14.5%; Score 241.5; DB 4; Length 369;  
Best Local Similarity 27.6%; Pred. No. 3.1e-12;  
Matches 96; Conservative 58; Mismatches 125; Indels 69; Gaps 14;

QY 3 PTISTLDTELPINGTEBTELCYKQTLSTLVLCI---VSLVGLTGNNAVIM-LIGCRMRR 58  
DB 16 PSPFDNGSLGPNNGSNGTEPYDMTNAVLTFYFVVCVGLCGNTLVIYIIRYAKMK 75  
QY 59 NAFSTIYIINLAADPLFLSGRLIYSLFSISIPH-----TISKILYPMMSYFAGLSFL 113  
DB 76 TITNIIYIINLAIDELFMIG--LPEFLANQVALVHMFSGKALCRVAVMTVDGINQFTSIFCL 133  
QY 114 SAVTERCISVLPIMYRCHRPHTLSAVVCVLLMALSLRSILEMML----- 160  
DB 134 TMSIDRIYLAIVHPIKSAKMRPRPAKMINVAVMGVSL-VILPIMIVAGLRSMQGRSS 192  
QY 161 CGFLFSGADSNACQTSPTTYAMLI-FL---CVLCCSSVLVLR---ILGSRKIPLT 212  
DB 193 CTINMPGSGAM--YTGFIYAFIIGFLVPLITICLCYLRITIKKSSGIVGSSKRRKS 250  
QY 213 RLIVYV--ILLTVLVFLGLPFGIOPLFLMTHVDREVLFCHVHVS----- 257  
DB 251 EKKVTRMVSIVAVVIFCMLP---FYIF-----NVSSVSAISPTPALKGMF 294  
QY 258 ---IFLSALNSSANPIIYFVFGSPRORONKMLKVLORALQDASEVD 302  
DB 295 DEVLIVLTANSKANPILVAFSLDNPKSPQNVLCIVKVSAGADGRSD 342

RESULT 15  
US-08-458-970A-10  
Sequence 10, Application US/08458970A  
Patent No. 5861272  
GENERAL INFORMATION:  
APPLICANT: LI, ET AL.  
TITLE OF INVENTION: C5a Receptor  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,970A  
FILING DATE: June 2, 1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/09234  
FILING DATE: 16 AUG 1994

ATTORNEY/AGENT INFORMATION:  
NAME: MULLINS, J.G.  
REGISTRATION NUMBER: 33,073  
REFERENCE/DOCKET NUMBER: 325800-353  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 364 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-458-970A-10

Query Match 14.2%; Score 236; DB 2; Length 364;  
Best Local Similarity 24.8%; Pred. No. 8.5e-12;  
Matches 84; Conservative 57; Mismatches 132; Indels 66; Gaps 13;

QY 32 VLTCTVSLVGLTGNNAVIMLLGCRMRRNAFSTIYIINLAADPLFLSGRLIYSLFSISIP 91  
DB 39 LIPAVTFVGLGNGGLVWVAGFRMHVTTTISYLNLAIDPCTFS-TLPFYIASVWVG 97  
QY 92 H-----TISKILYPMMSYFAGLSFSAVSTERCLSVLPIMYRCHRPHTLSAVVCVLL 146  
DB 98 HMFPGMCKEFTYTDINLFGSVFLIALIDRCICVLPVWQVNRFTVSLAKKVIIVP 157  
QY 147 WALSLRSILEMMLCGFLS-----GADSNACQTSDF-----I 179  
DB 158 W-----ICAFLLTLPTVIRLTTPVNSRLQPGKTAC-TFDFSPMTYDPEKKRV 204  
QY 180 TVAMLIPLCV--LCCSSVLILIRILC-----GSRKIPLTRLVYITLLTVLVFLC 228  
DB 205 AVTMLTVRGIRITIGFTSMISVALCYGLITKIHROGLKSSRLVLSFVAAFFLC 264  
QY 229 GLPFGIOPLFLMTHVDREVLFCHVHVSIF-----LSALNSSANPIIYFVG-SPRORQ 282  
DB 265 WCPFQV-VALLSTQYVERLKNMTPGIVTALKITSPLAFNSCLNMLYVFMQDPRERL 323  
QY 283 NRQNLKVLORAL-QDASEVDEGGQLPEIILESGSL 320  
DB 324 -IHSLPASLERALTEDSAQTSDTGTNLTGNTSLSENVL 361

Search completed: July 2, 2003, 19:23:15  
Job time : 15 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 2, 2003, 19:16:35 ; Search time 80 Seconds  
(without alignments)  
829.340 Million cells updates/sec

Title: US-09-849-869A-16

Sequence: 1 MDPRTSTLDTLTLPTINGTE.....EGGQQLPEETLHSGSLREQ 322

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

SPTREMBL 21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_proteol:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriophage:\*
- 17: sp\_archaeal:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1661	100.0	322	4	Q96LB2
2	1660	99.9	322	4	Q8TD8
3	1624	97.8	322	4	Q8TD8
4	1383	83.3	322	4	Q8TD8
5	1373	82.7	322	4	Q8TD8
6	1313	79.0	322	4	Q8TD8
7	1309	78.8	322	4	Q8TD8
8	1294	77.9	322	4	Q8TD8
9	1287	77.5	322	4	Q8TD8
10	1038.5	62.5	330	4	Q96LB1
11	847	51.0	337	11	Q8R4G1
12	821	49.4	338	11	Q91ZC2
13	769.5	46.3	338	11	Q91ZC3
14	761.5	45.8	331	11	Q91YB7
15	756.5	45.5	304	11	Q91WWS
16	735	44.3	302	11	Q91WWS

17	731.5	44.0	301	11	Q91ZC6	Q91ZC6 mus musculus
18	731.5	44.0	321	11	Q91ZC0	Q91ZC0 mus musculus
19	716.5	43.1	305	11	Q91ZC5	Q91ZC5 mus musculus
20	704.5	42.4	305	11	Q91ZC4	Q91ZC4 mus musculus
21	692.5	41.7	322	11	Q91ZB9	Q91ZB9 mus musculus
22	690.5	41.6	305	11	Q91WWS	Q91WWS mus musculus
23	687.5	41.4	313	11	Q91WWS	Q91WWS mus musculus
24	675	40.6	287	11	Q91ZC7	Q91ZC7 mus musculus
25	634	38.2	312	11	Q91ZC1	Q91ZC1 mus musculus
26	538.5	32.4	321	4	Q8TD8	Q8TD8 mus sapien
27	535.5	32.2	321	11	Q91ZB8	Q91ZB8 mus musculus
28	484	29.1	310	11	Q91ZB7	Q91ZB7 mus musculus
29	480.5	28.9	324	11	Q91ZC2	Q91ZC2 mus musculus
30	451	27.2	343	4	Q96AM1	Q96AM1 mus sapien
31	442.5	26.6	321	11	Q91WWS	Q91WWS mus musculus
32	416	25.0	319	11	Q91ZB6	Q91ZB6 mus musculus
33	416	25.0	343	11	Q8VCJ6	Q8VCJ6 mus musculus
34	349	21.0	289	11	Q91ZB5	Q91ZB5 mus musculus
35	253	15.2	390	13	Q8GQ4	Q8GQ4 catarrhini
36	250	15.1	351	11	Q88536	Q88536 mus musculus
37	248.5	15.0	343	11	Q88537	Q88537 mus musculus
38	247.5	14.9	355	6	Q91H1	Q91H1 macaca fasc
39	241.5	14.5	475	11	Q90MG9	Q90MG9 cavia porce
40	238	14.3	370	13	Q8UW5	Q8UW5 fugu rubrip
41	237.5	14.3	346	11	Q91Y73	Q91Y73 mus musculus
42	234.5	14.1	323	11	Q88538	Q88538 mus musculus
43	233.5	14.1	380	13	Q90GQ6	Q90GQ6 catarrhini
44	229.5	13.8	470	4	Q8TD2	Q8TD2 mus sapien
45	224	13.5	385	11	Q91K40	Q91K40 mus musculus

## ALIGNMENTS

RESULT 1

Q96LB2 PRELIMINARY; PRT; 322 AA.

AC Q96LB2; 01-DEC-2001 (TREMBL) 19, Created

DT 01-DEC-2001 (TREMBL) 19, Last sequence update

DT 01-JUN-2002 (TREMBL) 21, Last annotation update

DE G-protein-coupled receptor (putative G-protein coupled receptor).

GN MRCX1 OR GPCR.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE:11551509; PubMed:11551509;

RA Dong X., Han S.-K., Zyika M.-J., Simon M.I., Anderson D.B.,

RT "A Diverse Family of GPCRs Expressed in Specific Subsets of

RT Nociceptive Somatosensory Neurons."

RT Cell 106:619-632 (2001).

RN [2]

RP SEQUENCE FROM N.A.

RA Takeda S., Kadowaki S., Haga T., Takeasu H., Mitaku S.;

RT "Identification of G-protein-coupled receptor genes from the human

RT genome sequence."

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY042213; AKS1804.1; -

DR EMBL; AB083628; BAB89341.1; -

DR InterPro: IPR000276; GPCR\_Rhodopsin.

DR Pfam; PF00001; 7tm\_1; 1.

DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; UNKNOWN\_1.

DR PROSITE; PS00262; G\_PROTEIN\_RECP\_F1\_2; 1.

KW Receptor.

SO SEQUENCE 322 AA; 36250 MW; C7F3A9F418E8AD1 CRC64;

Query Match 100.0%; Score 1661; DB 4; Length 322;

Best Local Similarity 100.0%; Pred. No. 66-143;

Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MDPTSTLDTLPINGTEETLCYKQTLSTVLTCTIVSLVGTGNVAVMLGCRMRNA 60
DB 1 MDPTSTLDTLPINGTEETLCYKQTLSTVLTCTIVSLVGTGNVAVMLGCRMRNA 60
QY 61 FSIYILMLAADFLPLSGRLIYSLSTPHTISKILYPMVMSFYAGISFSAVSTER 120
DB 61 FSIYILMLAADFLPLSGRLIYSLSTPHTISKILYPMVMSFYAGISFSAVSTER 120
QY 121 CLSVLMPWIRCHRPHTLSAVVAVLWALSLRSILEMMLCGFLPSGADSAMCQTSDFIT 180
DB 121 CLSVLMPWIRCHRPHTLSAVVAVLWALSLRSILEMMLCGFLPSGADSAMCQTSDFIT 180
QY 181 VAMILFLCVLGCSSVLVLRILCGSRKIPLTRLYVTILLTVVFLICGPFQIOFFFL 240
DB 181 VAMILFLCVLGCSSVLVLRILCGSRKIPLTRLYVTILLTVVFLICGPFQIOFFFL 240
QY 241 WIHNDREVLFCGHVHVSIFLSALNSSANPITYFVGSFRORONKLVLOALODASE 300
DB 241 WIHNDREVLFCGHVHVSIFLSALNSSANPITYFVGSFRORONKLVLOALODASE 300
QY 301 VDEGGGQLPEEILBELSGRLRQ 322
DB 301 VDEGGGQLPEEILBELSGRLRQ 322

```

## RESULT 2

```

Q8TDD8 PRELIMINARY; PRT; 322 AA.
ID Q8TDD8
AC Q8TDD8;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE G protein-coupled receptor SNR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;
RN 11)
RP SEQUENCE FROM N.A.
RX MEDLINE=21853733; PubMed=11850634;
RA Lembo P.M., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
RA Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
RA Gosselin M., Fortin Y., Banville D., Shen S., Strom P., Payza K.,
RA Dray A., Walker P., Ahmad S.;
RA "Proenkephalin A gene products activate a new family of sensory
RT neuron-specific GPCRs."
RT Nat. Neurosci. 5:201-209 (2002).
DR EMBL: AF474989; AAL86881.1; -.
KW Receptor.
SQ SEQUENCE 322 AA; 36236 MW; C301BC174BB01D72 CRC64;

```

## Query Match

Best Local Similarity 99.9%; Score 1660; DB 4; Length 322;  
Matches 321; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MDPTSTLDTLPINGTEETLCYKQTLSTVLTCTIVSLVGTGNVAVMLGCRMRNA 60
DB 1 MDPTSTLDTLPINGTEETLCYKQTLSTVLTCTIVSLVGTGNVAVMLGCRMRNA 60
QY 61 FSIYILMLAADFLPLSGRLIYSLSTPHTISKILYPMVMSFYAGISFSAVSTER 120
DB 61 FSIYILMLAADFLPLSGRLIYSLSTPHTISKILYPMVMSFYAGISFSAVSTER 120
QY 121 CLSVLMPWIRCHRPHTLSAVVAVLWALSLRSILEMMLCGFLPSGADSAMCQTSDFIT 180
DB 121 CLSVLMPWIRCHRPHTLSAVVAVLWALSLRSILEMMLCGFLPSGADSAMCQTSDFIT 180
QY 181 VAMILFLCVLGCSSVLVLRILCGSRKIPLTRLYVTILLTVVFLICGPFQIOFFFL 240
DB 181 VAMILFLCVLGCSSVLVLRILCGSRKIPLTRLYVTILLTVVFLICGPFQIOFFFL 240
QY 241 WIHNDREVLFCGHVHVSIFLSALNSSANPITYFVGSFRORONKLVLOALODASE 300
DB 241 WIHNDREVLFCGHVHVSIFLSALNSSANPITYFVGSFRORONKLVLOALODASE 300

```

```

DB 241 WIHNDREVLFCGHVHVSIFLSALNSSANPITYFVGSFRORONKLVLOALODASE 300
QY 301 VDEGGGQLPEEILBELSGRLRQ 322
DB 301 VDEGGGQLPEEILBELSGRLRQ 322

```

## RESULT 3

```

Q8TDD9 PRELIMINARY; PRT; 322 AA.
ID Q8TDD9
AC Q8TDD9;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE G protein-coupled receptor SNR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;
RN 11)
RP SEQUENCE FROM N.A.
RX MEDLINE=21853733; PubMed=11850634;
RA Lembo P.M., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
RA Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
RA Gosselin M., Fortin Y., Banville D., Shen S., Strom P., Payza K.,
RA Dray A., Walker P., Ahmad S.;
RA "Proenkephalin A gene products activate a new family of sensory
RT neuron-specific GPCRs."
RT Nat. Neurosci. 5:201-209 (2002).
DR EMBL: AF474989; AAL86880.1; -.
KW Receptor.
SQ SEQUENCE 322 AA; 36300 MW; 6A1BB3D6EC7077B CRC64;

```

## Query Match

Best Local Similarity 97.8%; Score 1624; DB 4; Length 322;  
Matches 313; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

```

QY 1 MDPTSTLDTLPINGTEETLCYKQTLSTVLTCTIVSLVGTGNVAVMLGCRMRNA 60
DB 1 MDPTSTLDTLPINGTEETLCYKQTLSTVLTCTIVSLVGTGNVAVMLGCRMRNA 60
QY 61 FSIYILMLAADFLPLSGRLIYSLSTPHTISKILYPMVMSFYAGISFSAVSTER 120
DB 61 FSIYILMLAADFLPLSGRLIYSLSTPHTISKILYPMVMSFYAGISFSAVSTER 120
QY 121 CLSVLMPWIRCHRPHTLSAVVAVLWALSLRSILEMMLCGFLPSGADSAMCQTSDFIT 180
DB 121 CLSVLMPWIRCHRPHTLSAVVAVLWALSLRSILEMMLCGFLPSGADSAMCQTSDFIT 180
QY 181 VAMILFLCVLGCSSVLVLRILCGSRKIPLTRLYVTILLTVVFLICGPFQIOFFFL 240
DB 181 VAMILFLCVLGCSSVLVLRILCGSRKIPLTRLYVTILLTVVFLICGPFQIOFFFL 240
QY 241 WIHNDREVLFCGHVHVSIFLSALNSSANPITYFVGSFRORONKLVLOALODASE 300
DB 241 WIHNDREVLFCGHVHVSIFLSALNSSANPITYFVGSFRORONKLVLOALODASE 300
QY 301 VDEGGGQLPEEILBELSGRLRQ 322
DB 301 VDEGGGQLPEEILBELSGRLRQ 322

```

## RESULT 4

```

Q96LB0 PRELIMINARY; PRT; 322 AA.
ID Q96LB0
AC Q96LB0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE G protein-coupled receptor.
GN MRGX3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21435808; PubMed=11551509;  
RA Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.,  
RT "A Diverse Family of GPCRs Expressed in Specific Subsets of  
RT Nociceptive Somatosensory Neurons";  
RL Cell 106:619-632(2001).  
DR EMBL; AY042215; AAK91806.1; -.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KM Receptor.  
SQ SEQUENCE 322 AA; 36484 MW; 253B1BEF0CBAEB74 CRC64;  
Query Match 83.3%; Score 1383; DB 4; Length 322;  
Best Local Similarity 83.5%; Pred. No. 1,1e-117;  
Matches 269; Conservative 16; Mismatches 37; Indels 0; Gaps 0;  
QY 1 MDPSTLTDELTPINGTEETLCYKQTLSTVLTCTIVSLVGLTGNAAVLMGLGCRMRNA 60  
DB 1 MDPSTLPVLTGTELPINGRETEPCYKQTLSTVLTCTIVSLVGLTGNAAVLMGLGCRMRNA 60  
QY 61 FSIYIINLAADFLPSGRILYSLFSISPHITSKILYPMMSYFAGLSFSAVSTER 120  
DB 61 VSIYIINLVAAADFLPSGHILYSLFSISPHITSKILYPMMSYFAGLSFSAVSTER 120  
QY 121 CLSVLPPIWYHCRPHLSAVVCLVLMALSLRSILEMMLCGFLFGADSAMCOTSDFIT 180  
DB 121 CLSVLPPIWYHCRPHLSAVVCLVLMALSLRSILEMMLCGFLFGADSAMCOTSDFIT 180  
QY 181 VAMLIPLCVLCCSSVLVLRILCGSRKIPLTRLYTILTVLVFLCGLPFGIOFPL 240  
DB 181 IAWLVFLCVLCCSSVLVLRILCGSRKIPLTRLYTILTVLVFLCGLPFGIOFPL 240  
QY 241 WIHVDREVLFCVHVLVIFLSALNSSANPIYFVGSFRORONKLVLRALODPASE 300  
DB 241 RIHDMKVLFCVHVLVIFLSALNSSANPIYFVGSFRORONKLVLRALODPASE 300  
QY 301 VDEGGQGLPEIIELESGSRLEQ 322  
DB 301 VDEGGQGLPEIIELESGSRLEQ 322  
RESULT 5  
Q8TDE1 PRELIMINARY; PRT; 322 AA.  
AC Q8TDE1;  
DT 01-JUN-2002 (Tremblrel. 21, Created)  
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE G protein-coupled receptor SNR1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21853733; PubMed=11850634;  
RA Lembo P.M., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,  
RA Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier W., Labarre M.,  
RA Gosselin M., Fortin Y., Banville D., Shen S., Strom P., Payza K.,  
RA Dray A., Walker P., Ahmad S.;  
RT "Proenkephalin A gene products activate a new family of sensory  
RT neuron-specific GPCRs";  
RL Nat. Neurosci. 5:201-209(2002).  
DR EMBL; AF474987; AAL86878.1; -.  
KM Receptor.  
SQ SEQUENCE 322 AA; 36448 MW; 30A7F306F664D7 CRC64;  
Query Match 82.7%; Score 1373; DB 4; Length 322;

Best Local Similarity 82.0%; Pred. No. 8,6e-117;  
Matches 264; Conservative 22; Mismatches 36; Indels 0; Gaps 0;  
QY 1 MDPSTLTDELTPINGTEETLCYKQTLSTVLTCTIVSLVGLTGNAAVLMGLGCRMRNA 60  
DB 1 MDPSTLPVLTGTELPINGRETEPCYKQTLSTVLTCTIVSLVGLTGNAAVLMGLGCRMRNA 60  
QY 61 FSIYIINLAADFLPSGRILYSLFSISPHITSKILYPMMSYFAGLSFSAVSTER 120  
DB 61 VSIYIINLVAAADFLPSGHILYSLFSISPHITSKILYPMMSYFAGLSFSAVSTER 120  
QY 121 CLSVLPPIWYHCRPHLSAVVCLVLMALSLRSILEMMLCGFLFGADSAMCOTSDFIT 180  
DB 121 CLSVLPPIWYHCRPHLSAVVCLVLMALSLRSILEMMLCGFLFGADSAMCOTSDFIT 180  
QY 181 VAMLIPLCVLCCSSVLVLRILCGSRKIPLTRLYTILTVLVFLCGLPFGIOFPL 240  
DB 181 IAWLVFLCVLCCSSVLVLRILCGSRKIPLTRLYTILTVLVFLCGLPFGIOFPL 240  
QY 241 WIHVDREVLFCVHVLVIFLSALNSSANPIYFVGSFRORONKLVLRALODPASE 300  
DB 241 RIHDMKVLFCVHVLVIFLSALNSSANPIYFVGSFRORONKLVLRALODPASE 300  
QY 301 VDEGGQGLPEIIELESGSRLEQ 322  
DB 301 VDEGGQGLPEIIELESGSRLEQ 322  
RESULT 6  
Q8TDE0 PRELIMINARY; PRT; 322 AA.  
AC Q8TDE0;  
DT 01-JUN-2002 (Tremblrel. 21, Created)  
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE G protein-coupled receptor SNR2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21853733; PubMed=11850634;  
RA Lembo P.M., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,  
RA Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier W., Labarre M.,  
RA Gosselin M., Fortin Y., Banville D., Shen S., Strom P., Payza K.,  
RA Dray A., Walker P., Ahmad S.;  
RT "Proenkephalin A gene products activate a new family of sensory  
RT neuron-specific GPCRs";  
RL Nat. Neurosci. 5:201-209(2002).  
DR EMBL; AF474988; AAL86879.1; -.  
KM Receptor.  
SQ SEQUENCE 322 AA; 36551 MW; CE42431FD3B4611B CRC64;  
Query Match 79.0%; Score 1313; DB 4; Length 322;  
Best Local Similarity 80.1%; Pred. No. 2,4e-111;  
Matches 257; Conservative 21; Mismatches 43; Indels 0; Gaps 0;  
QY 1 MDPSTLTDELTPINGTEETLCYKQTLSTVLTCTIVSLVGLTGNAAVLMGLGCRMRNA 60  
DB 1 MDPSTLPVLTGTELPINGRETEPCYKQTLSTVLTCTIVSLVGLTGNAAVLMGLGCRMRNA 60  
QY 61 FSIYIINLAADFLPSGRILYSLFSISPHITSKILYPMMSYFAGLSFSAVSTER 120  
DB 61 VSIYIINLVAAADFLPSGHILYSLFSISPHITSKILYPMMSYFAGLSFSAVSTER 120  
QY 121 CLSVLPPIWYHCRPHLSAVVCLVLMALSLRSILEMMLCGFLFGADSAMCOTSDFIT 180  
DB 121 CLSVLPPIWYHCRPHLSAVVCLVLMALSLRSILEMMLCGFLFGADSAMCOTSDFIT 180  
QY 181 VAMLIPLCVLCCSSVLVLRILCGSRKIPLTRLYTILTVLVFLCGLPFGIOFPL 240  
DB 181 IAWLVFLCVLCCSSVLVLRILCGSRKIPLTRLYTILTVLVFLCGLPFGIOFPL 240

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QY 241 WIHDEVLFCHVHLSIFLSALNSSANPIIFVFGSFROKRONKLVLOALQDASE 300
DB 241 RIHIDMWLVLFCHVHLSIFLSALNSSANPIIFVFGSFROKRONKLVLOALQDASE 300
QY 301 VDEGGQGLPEEILFELSGSRL 321
DB 301 VDEGGQGLPEEILFELSGSRL 321

RESULT 7
Q8TDD7 PRELIMINARY; PRT; 322 AA.
AC Q8TDD7;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE G protein-coupled receptor SNRS5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21853733; PubMed=11850634;
RA Lembo P.M., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
RA Zhang J., Hofert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
RA Gosselin M., Fortin Y., Barville D., Shen S., Strom P., Paya K.,
RA Dray A., Walker P., Ahmad S.;
RT "Proenkephalin A gene products activate a new family of sensory
RT neuron-specific GPCRs."
RL Nat. Neurosci. 5:201-209(2002).
RM EMBL; AF474991; AAL86882.1; -.
KW Receptor.
SQ SEQUENCE 322 AA; 36423 MW; 306FBA5DDFDD90 CRC64;

Query Match 78.8%; Score 1309; DB 4; Length 322;
Best Local Similarity 80.3%; Pred. No. 5.6e-111;
Matches 257; Conservative 20; Mismatches 43; Indels 0; Gaps 0;

QY 1 MDPTISTLDTELPINGTEETLCYKQTLSTLVLTCTVSLSVGLTGNVAVLMLGCRMRNA 60
DB 1 MDPTVPVFGTKLPINGREETPCYKQTLSTLVLTCTVSLSVGLTGNVAVLMLGCRMRNA 60
QY 61 FSIYIINLAADFLFSGRLIYSLFISIPHTISKILPYMMFSYFAGISFLSAVSTER 120
DB 61 VSIYIINLAADFLFSGRLIYSLFISIPHTISKILPYMMFSYFAGISFLSAVSTER 120
QY 121 CLSVLMPITWRCHRPHTLSAVVCVLLMALSLRSILEMMLCGFLFGADSAMCOTSDPIT 180
DB 121 CLSVLMPITWRCHRPHTLSAVVCVLLMALSLRSILEMMLCGFLFGADSAMCOTSDPIT 180
QY 181 VAMLIPLFCVLCGSSVLILRLCGSRKIPLTRLYVTILLTVLVFLCGLPFGIOFFEL 240
DB 181 VAMLIPLFCVLCGSSVLILRLCGSRKIPLTRLYVTILLTVLVFLCGLPFGIOFFEL 240
QY 241 WIHDEVLFCHVHLSIFLSALNSSANPIIFVFGSFROKRONKLVLOALQDASE 300
DB 241 RIHIDMWLVLFCHVHLSIFLSALNSSANPIIFVFGSFROKRONKLVLOALQDASE 300
QY 301 VDEGGQGLPEEILFELSGSRL 320
DB 301 VDEGGQGLPEEILFELSGSRL 320

RESULT 8
Q96LA9 PRELIMINARY; PRT; 322 AA.
AC Q96LA9;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE G protein-coupled receptor.
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GN MRG4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21435808; PubMed=11551509;
RA Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
RT "A diverse family of GPCRs expressed in specific subsets of
RT nociceptive Somatosensory Neurons."
RL Cell 106:619-632(2001).
RM EMBL; AY042216; AAK91807.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1.1.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 36434 MW; 7CA676F8BD390A31 CRC64;

Query Match 77.9%; Score 1294; DB 4; Length 322;
Best Local Similarity 79.7%; Pred. No. 1.3e-109;
Matches 255; Conservative 20; Mismatches 45; Indels 0; Gaps 0;

QY 1 MDPTISTLDTELPINGTEETLCYKQTLSTLVLTCTVSLSVGLTGNVAVLMLGCRMRNA 60
DB 1 MDPTVPVFGTKLPINGREETPCYKQTLSTLVLTCTVSLSVGLTGNVAVLMLGCRMRNA 60
QY 61 FSIYIINLAADFLFSGRLIYSLFISIPHTISKILPYMMFSYFAGISFLSAVSTER 120
DB 61 VSIYIINLAADFLFSGRLIYSLFISIPHTISKILPYMMFSYFAGISFLSAVSTER 120
QY 121 CLSVLMPITWRCHRPHTLSAVVCVLLMALSLRSILEMMLCGFLFGADSAMCOTSDPIT 180
DB 121 CLSVLMPITWRCHRPHTLSAVVCVLLMALSLRSILEMMLCGFLFGADSAMCOTSDPIT 180
QY 181 VAMLIPLFCVLCGSSVLILRLCGSRKIPLTRLYVTILLTVLVFLCGLPFGIOFFEL 240
DB 181 VAMLIPLFCVLCGSSVLILRLCGSRKIPLTRLYVTILLTVLVFLCGLPFGIOFFEL 240
QY 241 WIHDEVLFCHVHLSIFLSALNSSANPIIFVFGSFROKRONKLVLOALQDASE 300
DB 241 RIHIDMWLVLFCHVHLSIFLSALNSSANPIIFVFGSFROKRONKLVLOALQDASE 300
QY 301 VDEGGQGLPEEILFELSGSRL 320
DB 301 VDEGGQGLPEEILFELSGSRL 320

RESULT 9
Q8TDD6 PRELIMINARY; PRT; 322 AA.
AC Q8TDD6;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE G protein-coupled receptor SNRS6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21853733; PubMed=11850634;
RA Lembo P.M., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,
RA Zhang J., Hofert C., Cao J., Schmidt R., Pelletier M., Labarre M.,
RA Gosselin M., Fortin Y., Barville D., Shen S., Strom P., Paya K.,
RA Dray A., Walker P., Ahmad S.;
RT "Proenkephalin A gene products activate a new family of sensory
RT neuron-specific GPCRs."
RL Nat. Neurosci. 5:201-209(2002).
RM EMBL; AF474992; AAL86883.1; -.
KW Receptor.
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SO SEQUENCE 322 AA; 36434 MW; 7CA6658D70548BA CRC64;  
Query Match 77.5%; Score 1287; DB 4; Length 322;  
Best Local Similarity 79.1%; Pred. No. 5.5e-109;  
Matches 253; Conservative 21; Mismatches 46; Indels 0; Gaps 0;  
QY 1 MDPTISTLDTELPIINGTEETLCYKOTLSLVTVTCIVSVLGTGNVAVLMLGCRMRNA 60  
DB 1 MDPTVPVFGKLTPIINGTEETPCYNQTLSTFVLCIISLVGLTGNVAVLMLGCRMRNA 60  
QY 61 FSIYIINLAADFLFSGRLIYSLFISIPHTISKILPYVMFSPYAGLSFAVSTER 120  
DB 61 VSIYIINLAADFLFSGRLIYSLFISIPHTISKILPYVMFSPYAGLSFAVSTER 120  
QY 121 CLSTVLMPIWRCRPHLSAVVAVLMLSLRSILEMMLCGFLPSGADSAMCOTSPIT 180  
DB 121 CLSTVLMPIWRCRPHLSAVVAVLMLSLRSILEMMLCGFLPSGADSAMCOTSPIT 180  
QY 181 VAMLIPLCVLVCSSSLVLLIRILCGSRKIPLTRLYVTILLTVVFLCGIPFGIQLFL 240  
DB 181 VAMLIPLCVLVCSSSLVLLIRILCGSRKIPLTRLYVTILLTVVFLCGIPFGIQLFL 240  
QY 241 WIHVREVLFCVHVLVSIPLSALNSSANPIIYFVSGFRORONKLVLRALQDASE 300  
DB 241 RMHLNLEVLVCHVYLVGMSLSLSSANPIIYFVSGFRORONKLVLRALQDASE 300  
QY 301 VDDEGQGLPEEILFSGSRL 320  
DB 301 VDKEGQGLPEEILFSGSRL 320  
- RESULT 10  
Q96LB1 PRELIMINARY; PRT; 330 AA.  
AC Q96LB1;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE G-protein-coupled receptor (Putative G-protein coupled receptor).  
GN MGX2 OR GPCR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21435808; PubMed=11551509;  
RA Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;  
RT "A Diverse Family of GPCRs Expressed in Specific Subsets of  
RT Nociceptive Somatosensory Neurons.";  
RT Cell 106:619-632 (2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;  
RT "Identification of G protein-coupled receptor genes from the human  
RT genome sequence.";  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY042214; AAK91805.1; -;  
DR EMBL: AB083626; BAB89339.1; -;  
DR InterPro: IPR000276; GPCR\_Rhodopsin.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PROSITE: PS00237; G\_PROTEIN\_RECEPTOR\_1; UNKNOWN\_1.  
DR PROSITE: PS50262; G\_PROTEIN\_RECEPTOR\_1; 1.  
KM RECEPTOR.  
SQ SEQUENCE 330 AA; 37099 MW; 0B328FD78BD1D66E CRC64;  
Query Match 62.5%; Score 1038.5; DB 4; Length 330;  
Best Local Similarity 64.7%; Pred. No. 2.1e-86;  
Matches 213; Conservative 27; Mismatches 80; Indels 9; Gaps 3;  
QY 1 MDPTISTLDTELPIINGTEETLCYKOTLSLVTVTCIVSVLGTGNVAVLMLGCRMR 57  
DB 1 MDPTVPVFGKLTPIINGTEETPCYNQTLSTFVLCIISLVGLTGNVAVLMLGCRMR 60

QY 58 RNAPSYIINLAADFLFSGRLIYSL----SFISIPHTISKILPYVMFSPYAGLSFL 113  
DB 61 RNAPSYIINLAADFLFSGRLIYSL----SFISIPHTISKILPYVMFSPYAGLSFL 120  
QY 114 SAVTERCISLVMPWRCRPHLSAVVAVLMLSLRSILEMMLCGFLPSGADSAMC 173  
DB 121 STVSTERCISLVMPWRCRPHLSAVVAVLMLSLRSILEMMLCGFLPSGADSAMC 180  
QY 174 QTSDFITVAMLIPLCVLVCSSSLVLLIRILCGSRKIPLTRLYVTILLTVVFLCGIPFG 233  
DB 181 QTSDFITVAMLIPLCVLVCSSSLVLLIRILCGSRKIPLTRLYVTILLTVVFLCGIPFG 240  
QY 234 IOFFFLMIVHDEVLFCVHVLVSIPLSALNSSANPIIYFVSGFRORONK-LKVL 291  
DB 241 IOFFFLMIVHDEVLFCVHVLVSIPLSALNSSANPIIYFVSGFRORONK-LKVL 300  
QY 292 QRALQDASEVDDEGQGLPEEILFSGSRL 320  
DB 301 QRALQDASEVDDEGQGLPEEILFSGSRL 329

- RESULT 11  
Q984G1 PRELIMINARY; PRT; 337 AA.  
AC Q984G1;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE G-protein-coupled receptor SNR.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY;  
RX MEDLINE=21853733; PubMed=11650634;  
RA Lembo P.M., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,  
RA Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,  
RA Gosselin M., Fortin Y., Banville D., Shen S., Strom P., Payza K.,  
RA Dray A., Walker P., Ahmad S.;  
RT "Proenkephalin A gene products activate a new family of sensory  
RT neuron-specific GPCRs.";  
RL Nat. Neurosci. 5:201-209 (2002).  
DR EMBL: AF474986; AAL86877.1; -;  
KM RECEPTOR.  
SQ SEQUENCE 337 AA; 38702 MW; B8D72ED92C65E2A CRC64;  
Query Match 51.0%; Score 847; DB 11; Length 337;  
Best Local Similarity 53.4%; Pred. No. 5.3e-69;  
Matches 172; Conservative 48; Mismatches 92; Indels 10; Gaps 5;  
QY 1 MDPTISTLDTELPIINGTEETLCYKOTLSLVTVTCIVSVLGTGNVAVLMLGCRMRNA 60  
DB 15 MDPTISTLDTELPIINGTEETLCYKOTLSLVTVTCIVSVLGTGNVAVLMLGCRMRNA 73  
QY 61 FSIYIINLAADFLFSGRLIYSLFISIPHTISKILPYVMFSPYAGLSFAVSTER 115  
DB 61 FSIYIINLAADFLFSGRLIYSLFISIPHTISKILPYVMFSPYAGLSFAVSTER 123  
QY 121 CLSTVLMPIWRCRPHLSAVVAVLMLSLRSILEMMLCGFLPSGADSAMCOTSPIT 175  
DB 121 CLSTVLMPIWRCRPHLSAVVAVLMLSLRSILEMMLCGFLPSGADSAMCOTSPIT 192  
QY 176 SDFITVAMLIPLCVLVCSSSLVLLIRILCGSRKIPLTRLYVTILLTVVFLCGIPFG 235  
DB 193 VDFITVAMLIPLCVLVCSSSLVLLIRILCGSRKIPLTRLYVTILLTVVFLCGIPFG 252  
QY 236 FFLFVLMIVHDEVLFCVHVLVSIPLSALNSSANPIIYFVSGFRORONKLVLRAL 295  
DB 253 LFLFVLMIVHDEVLFCVHVLVSIPLSALNSSANPIIYFVSGFRORONKLVLRAL 312

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QY 296 QDASEVDE---GGGOLPEEIE 314
DB 313 EEPDEDEYTDSDVOKPELISE 334

RESULT 12
ID Q91ZC2 PRELIMINARY; PRT; 338 AA.
AC Q91ZC2;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE G-protein-coupled receptor.
GN MRB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;

[1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=21435808; PubMed=11551509;
RA Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
RT "A Diverse Family of GPCRs Expressed in Specific Subsets of
RT Nociceptive Somatosensory Neurons."
RL Cell 106:619-632(2001).
DR EMBL; AY042200; AAK91796.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 338 AA; 38832 MW; 1B0A091D67C668B9 CRC64;

Query Match 49.4%; Score 821; DB 11; Length 338;
Best Local Similarity 51.4%; Pred. No. 1.2e-66;
Matches 164; Conservative 51; Mismatches 92; Indels 12; Gaps 4;

QY 6 STDLELTPINGT---ETLCYKQTLSTVLTCTVSLVGLTGNVAVLMLGCRNRNFS 62
DB 13 SAMKINIVLVNGSYVIDTSCVTRNOAMILLIISLVGMGINAVIMFLGIRHNTAFT 72
QY 63 IYIINLAADPLFLSGRLIYSL---SFISIPHTISKILYPMVMFSYFAGISFSAVST 118
DB 73 VYIINLAADPLFLYCSQVITCLLAFTFYISIDINIPVLVYVPIFAVLSGLISTSTI 132
QY 119 ERCLSVLPIMYRCHPHTLSAVVCLLMALSLSLLEWMLCGFLFSGADSAMQTSDF 178
DB 133 ERCLSVLPIMYRCHPHTLSAVVCLLMALSLSLLEWMLCGFLFSGADSAMQTSDF 192
QY 179 ITVAMLIPLCVLTCGSSVLVLRILICGSRKIPLTRLYTILLTVVFLCGLPRIQFPL 238
DB 193 ITNINSVFPGVLCSSSLTLVLRIFCGSORIPMTSLYVITLVVFLIFGLPFIYVIL 252
QY 229 FLMIHVDEYLFCHVHLVSIPLSALNSSANPIYFVGSFQRO-NRONLKLIVLORAD 297
DB 253 YQMSNFYVEICNFTLEILFLSCVNSCMPITLYVGSIRRRRRKTKLLORAD 312
QY 298 ASEVDEGG---GQLPEEI 312
DB 313 TPBEQSGNKSSEPEEL 331

RESULT 13
ID Q91ZC3 PRELIMINARY; PRT; 338 AA.
AC Q91ZC3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE G-protein-coupled receptor.
GN MRGB1.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;

[1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=21435808; PubMed=11551509;
RA Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.;
RT "A Diverse Family of GPCRs Expressed in Specific Subsets of
RT Nociceptive Somatosensory Neurons."
RL Cell 106:619-632(2001).
DR EMBL; AY042199; AAK91795.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 338 AA; 38750 MW; 9597037ED0BE8CE5 CRC64;

Query Match 46.3%; Score 769.5; DB 11; Length 338;
Best Local Similarity 49.5%; Pred. No. 5.9e-62;
Matches 160; Conservative 49; Mismatches 103; Indels 11; Gaps 4;

QY 1 MDPLTSLDLELTPINGTER---TLCYKQTLSTVLTCTVSLVGLTGNVAVLMLGCRNR 57
DB 1 MDLVLDWTINITALKESNDNGISFCEVWSRTMTFLSLIALVGLGNATVLMFLGQNS 60
QY 58 RNAFSYIINLAADPLFLSGRLI---YSLSTISIPHTISKILYPMVMFSYFAGISFSL 114
DB 61 RNAFSYIINLAADPLFLSGRLI---YSLSTISIPHTISKILYPMVMFSYFAGISFSL 120
QY 115 AVSTERCLSVLPIMYRCHPHTLSAVVCLLMALSLSLLEWMLCGFLFSGADSAMQ 174
DB 121 VISTERCLSVLPIMYRCHPHTLSAVVCLLMALSLSLLEWMLCGFLFSGADSAMQ 180
QY 175 TSDPLTAVMLIPLCVLTCGSSVLVLRILICGSRKIPLTRLYTILLTVVFLCGLPFI 234
DB 181 TFDPLTAVMLIPLCVLTCGSSVLVLRILICGSRKIPLTRLYTILLTVVFLCGLPFI 240
QY 235 QFLFLMIHVDEYLFCHVHLVSIPLSALNSSANPIYFVGSFQRO-NRONLKLIVLOR 293
DB 241 QFLFLMIHVDEYLFCHVHLVSIPLSALNSSANPIYFVGSFQRO-NRONLKLIVLOR 300
QY 294 ALQDASEVDE---GGGOLPEEI 312
DB 301 AMQDSEBECEGMSGSSRPREI 323

RESULT 14
ID Q91YB7 PRELIMINARY; PRT; 331 AA.
AC Q91YB7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE G-protein coupled receptor.
GN RC 56.1.3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxId=10116;

[1]
SEQUENCE FROM N.A.
RA Bender E.;
RT "Cloning and functional characterization of the rat orphan GPCR
RT rc 56.1.3."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ311952; CAC84592.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor.

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SQ SEQUENCE 331 AA; 37005 MW; 7ABA8C557859AC CRC64;  
 Query Match 45.8%; Score 761.5; DB 11; Length 331;  
 Best Local Similarity 51.0%; Pred. No. 3,1e-61;  
 Matches 172; Conservative 39; Mismatches 91; Indels 35; Gaps 7;  
 QY 1 MDPITSLD-TELPINGTEETLCYKQTLSTVLTCTVSLVGLTGNVVMGLGCRNRN 59  
 DB 13 LMSASTIAVATTNPMCKTIPGSGNKRLLPNLIIISGLVGLGNAMVFWLGLFRLARN 72  
 QY 60 AFSYIILNLAADFLPLSGRLVSLSPISIPHTISKILY-----VMMFSYFAG 109  
 DB 73 AFSYIILNLAADFLPLCHTIDSTLL-----KFSYNIIFLPCENVMVWPYIAG 125  
 QY 110 LSPISAVSTERCLSVLPWYRCHRPHTLSANVCVLMALSLSRILEMILCGFLFGAD 169  
 DB 126 LMSLSAISTERCLSVCPPIWYRCRPPKHTSTMCSAIVLSLLCIINRFYCGFL----D 181  
 QY 170 SAW-----CQTSDFITAMLIIFLCVLCGSSVLVLIILGSRKIPLTRVYTTLLTVLV 224  
 DB 182 TKYKDNRCCLASNFETPACLIFLVVLCSSLLALVRSFCGAGMKLRLVATTMLTLV 241  
 QY 225 FLGLGPFQIOFPLFLWHDREVLFGVHLVSIPLSALNSANPIYFVGSFRQRNR 284  
 DB 242 FLGLGPFQIHFVFLIWKIDYKFAVGLYLAALVLTAVNSCANPIYFVGSFR-HQKH 300  
 QY 285 QNLKLVQRALQDASEVDEGGQLPPEILEISGRLE 321  
 DB 301 QTLKMLQRALQDTPET-----AENTVEMSSKVE 330

## RESULT 15

Q91WMS PRELIMINARY; PRT; 304 AA.  
 AC Q91WMS;

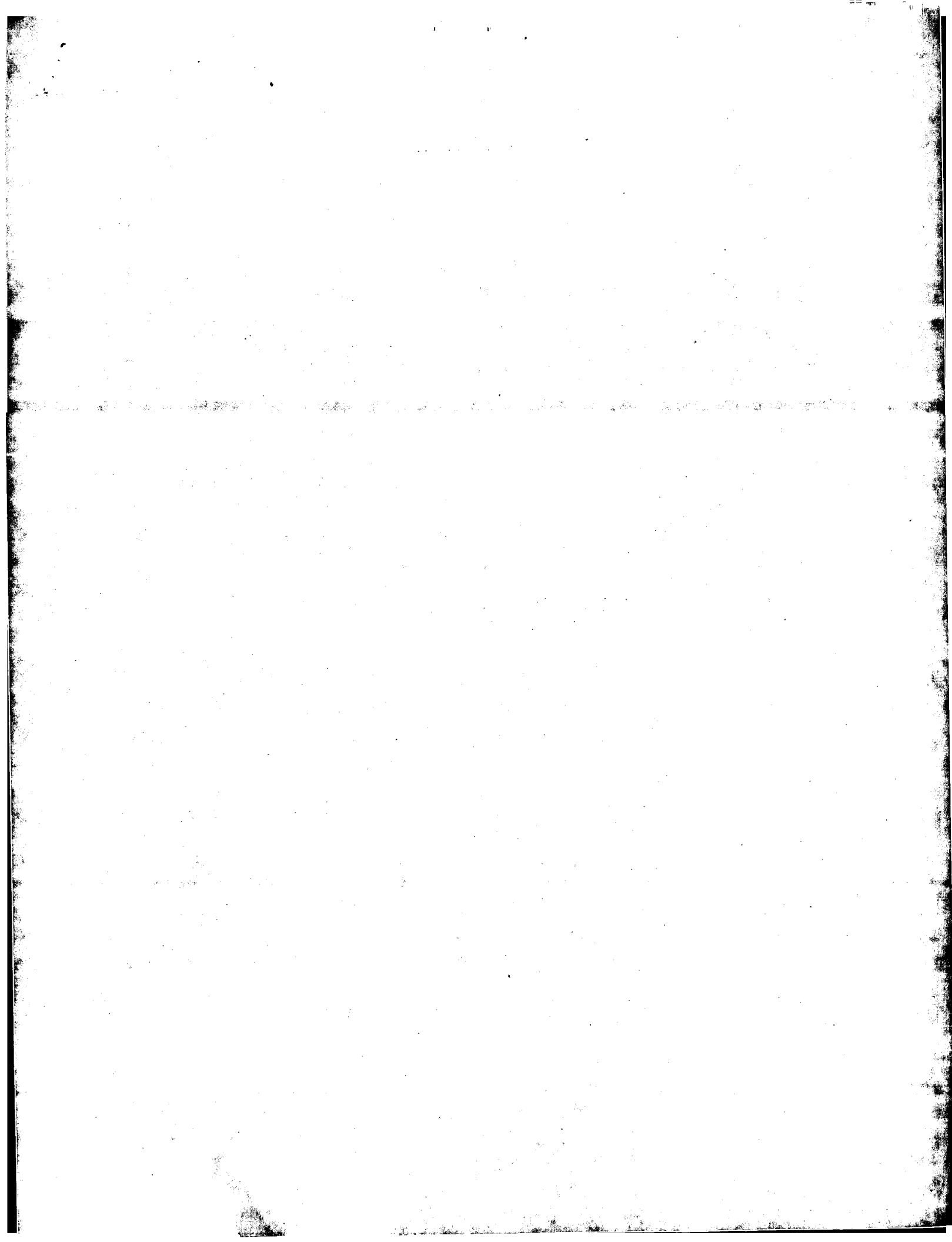
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE RF-amide G protein-coupled receptor.  
 GN MRGAL.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=DORSAL ROOT GANGLION;  
 RX MEDLINE=21435808; PubMed=11551509;  
 RA Dong X., Han S., Zyika M.J., Simon M.I., Anderson D.J.;  
 RT "A diverse family of spcres expressed in specific subsets of  
 nociceptive sensory neurons."  
 RL Cell 106:619-632 (2001)  
 DR EMBL: AY042191; AAK91787.1; -  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KM Receptor  
 SQ SEQUENCE 304 AA; 34381 MW; C56CBF879067A52B CRC64;

Query Match 45.5%; Score 756.5; DB 11; Length 304;  
 Best Local Similarity 53.0%; Pred. No. 8e-61;  
 Matches 160; Conservative 43; Mismatches 84; Indels 15; Gaps 4;

QY 28 LSLTVL-----TCVSLVGLTGNVVMGLGCRNRNFAFSYIILNLAADFLPLSGRLIY 82  
 DB 9 INITILIPNMIILFGLVGLTGNVFWLGLFCILHRNFAFSYIILNLAADFFFLGHIID 68  
 QY 83 SLSPISIPHTISKIL--YPMFMSYFAGLSFLSAVSTERCLSVLPWYRCHRPHTLSA 140  
 DB 69 SILLNLNVFYPIITLFCFTYIMVLYTAGLSLSAISTERCLSVLCPIWYCHRPHTST 128  
 QY 141 VCVLLMALSLRSILEMILCGFLFG-ADSAMCQTSDFITVAVLIFLCVVLGSSSLVLL 199

DB 129 VMCAVIMVLSLLICINSYFCGFLNTQYKNENGCLALNFTTAIVLMPFLVVLCLSSIALV 188  
 QY 200 IRIICGRKIPLTRVYTTLLTVLVFLCGLPFGIOFPLWHDREVLFGVHLVSIIF 259  
 DB 189 ARIFCGGQIKLRLVYTTIISLVFLCGLPFGIHFVFLFKDKDFHVDLGFYLASV 248  
 QY 260 LSLNSANPIYFVGSFRQRNRQNLKVLQRALQDASEVDEGGQLPPEILEISGR 319  
 DB 249 LTAINSCANPIYFVGSFRRLKHQTLKVLQNALQDTPET-----AKIMVEMSRSK 301  
 QY 320 LE 321  
 DB 302 SE 303

Search completed: July 2, 2003, 19:22:29  
 Job time : 82 secs







FT DOMAIN 284 324 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 5 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 16 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 21 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 324 AA; 37130 MW; AD810229BF1E7D36 CRC64;  
 Query Match 29.2%; Score 484.5; DB 1; Length 324;  
 Best Local Similarity 39.2%; Pred. No. 1.9e-25;  
 Matches 112; Conservative 61; Mismatches 86; Indels 27; Gaps 10;  
 QY VSLVGLGNNAVWMLGCRMRNPFSTYIINLAADFLPSGRII-----YLSLSFISIP 92  
 Db 41 ISPLGFVENGLLWFLFCFRMRNPPYITHTLSADISLFCITILSIDYALDYELSSG 100  
 QY TISKLIVPV-MMFSYFAGLSFSLAVSTERCLSLVMPIMYRCHRPHTLSAVVCVLLMALSL 151  
 Db 101 YTTIVTLVTLFPGNGLVLTALISVERCLSVLYPIWYRCHRPKHQSAFVLCALMALSLC 160  
 QY 152 LRSILFEMWLCGLFSGADSAMCQTS-----FTTV-AMLIPLCVLGGSSVLLIRILC 204  
 Db 161 LVTIMFVWC--ISGESH--SOSDCRAVILFALISFLVFTPLMLV-SSTILVXIRK 215  
 QY 205 GSRKIPRLRLVYTLITLVFLVFLCGLPFGIOPLF--LMHVDREVLFCHVHLVSIFLSA 262  
 Db 216 NTWASHSKLYIVWVITIIIFLIPAMPKRVLYLYEYV-----STGNINHSILFST 269  
 QY 263 LNSSANPIYFVFGSFRQRNRONIKLVLRALODASEV--DEGGG 306  
 Db 270 INSSANPIYFVFGSKKKRFRESLKVLTFAFKDEMPPRQEGNG 315  
 RESULT 2  
 MSG\_HUMAN STANDARD; PRT; 378 AA.  
 AC P35110;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-OCT-2002 (Rel. 41, Last annotation update)  
 DE MAS-related G protein-coupled receptor MSG.  
 GN MSG.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OK NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92130997; PubMed=1723144;  
 RA Monnot C., Weber V., Stimakre J., Bihoreau C., Teutsch B., Corvol P.,  
 RA Clausen E.;  
 RT "Cloning and functional characterization of a novel mas-related gene,  
 RT modulating intracellular angiotensin II actions.";  
 RT Mol. Endocrinol. 5:1477-1487(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Whitaker H.;  
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC MOST SIMILAR TO MAS.  
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 CC -----  
 DR EMBL: S78653; AAB21255.1; -  
 DR EMBL: AL035542; CAB44503.1; -  
 DR PIR: A39485; A39485.  
 DR InterPro: IPR000276; GPCR\_Rhodopsin.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEPT\_F1\_1. 1.

DR PROSITE: PS00262; G\_PROTEIN\_RECEPT\_F1\_2. 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 77  
 FT TRANSMEM 78 101  
 FT TRANSMEM 102 109  
 FT TRANSMEM 110 136  
 FT TRANSMEM 137 154  
 FT TRANSMEM 155 169  
 FT TRANSMEM 170 191  
 FT TRANSMEM 192 207  
 FT TRANSMEM 208 221  
 FT TRANSMEM 222 248  
 FT TRANSMEM 249 264  
 FT TRANSMEM 265 286  
 FT TRANSMEM 287 297  
 FT TRANSMEM 298 317  
 FT TRANSMEM 318 378  
 FT CARBOHYD 54 54  
 FT CARBOHYD 57 57  
 SQ SEQUENCE 378 AA; 42410 MW; E08A606294B61474 CRC64;  
 Query Match 27.8%; Score 462; DB 1; Length 378;  
 Best Local Similarity 37.4%; Pred. No. 6.6e-24;  
 Matches 114; Conservative 56; Mismatches 101; Indels 34; Gaps 9;  
 QY 16 NGTEETL-----CYKQTLSTLV--TCIYSLVGLTGNAAVWMLGCRMRNPFSTYI 65  
 Db 54 NEINETIHHQMSAAVQOALPNIITAPKAVLVLGVLNGTVFMLCCG-ATNPYMYI 112  
 QY 66 LNLAAFLFLS---GRILYSLSTSLPHITISKLIVVMMFSYFAGLSFSLAVSTERC 121  
 Db 113 LHLVADVILYCCSAGVFLQVTLTYHGAVFFLPFLALISPSFEVCLCLVAISTERC 172  
 QY 122 LSLVLPWYRCHRPHTLSAVVCVLLMALSLRSILEMWCGLFSGADSAMCQTS---F 178  
 Db 173 VCVLPFWYRCHRPKTSNVCTIWLGLPCINIVSLVLY-----WGHVACVIF 224  
 QY 179 ITVAMLI--FLCVLGGSSVLLIRILGSRKIPRLVYTLITLVFLVFLCGLPFGIOF 236  
 Db 225 LKLSGLFHALSLVWCSSITLIRFLCCSQOQKARVAVVQISAPMFLMLPLSVAP 284  
 QY 237 FLFLMIVHDEVYFCHVHLVSTLSANSNANPIYFVFGSFRQRNRONIKLVLRALQ 296  
 Db 285 LI-----TDFKMFVTTLSYLSLFL-IINSNANPIYFVGSJRKRLKESLRVTLQRAL 338  
 QY 297 DASEV 301  
 Db 339 DKPEV 343  
 RESULT 3  
 MAS\_HUMAN STANDARD; PRT; 325 AA.  
 ID P04201;  
 DT 20-MAR-1987 (Rel. 04, Created)  
 DT 20-MAR-1987 (Rel. 04, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE MAS proto-oncogene.  
 GN MAS1 OR MAS.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OK NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86218084; PubMed=3708691;  
 RA Young D., Walches G., Bitchmeier C., Fasano O., Wigler M.;  
 RT "Isolation and characterization of a new cellular oncogene encoding a  
 RT protein with multiple potential transmembrane domains.";  
 RT Cell 45:711-719(1986).  
 RN [2]  
 RP POSSIBLE FUNCTION.  
 RX MEDLINE=86334724; PubMed=3419518;



FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 19 19 S -> I (IN REF. 2).  
 SQ SEQUENCE 324 AA; 36904 MW; 24F4AB7299E6016F CRC64;  
 Query Match 27.5%; Score 456.5; DB 1; Length 324;  
 Best Local Similarity 38.1%; Pred. No. 1.3e-23; Indels 27; Gaps 10;  
 Matches 109; Conservative 61; Mismatches 89;  
 QY VSLVGLGNNAVVLMLGCMRRNRFSTIYILNLAADFLSGRLIYSLFSLSPH 92  
 DB 41 ISPLGFEVNGILMLFLCFRRMRNPFTYITLMSADSLFCPIILSIDVALDEHSSGH 100  
 QY 93 TISKILYPV-MPESYFAGLSFSAVSTERCISVLPWYRCHPETHSAVVCVLLMALSL 151  
 DB 101 HYTVLTVLTVFLFPGVNGLYLITLTAISVERCLSVLPWYSHRKHQSAFVLCALLALSC 160  
 QY 152 LRSILEMMLGFLFSGADSAWCQSD-----FTTV-AMILFCVLCGSSVLVILRLIC 204  
 DB 161 LVTTMEYVMC--IDSGESH--SRSDCAVITIFALLSFLVFTPLMLVSS--ILVVKIRK 215  
 QY 205 GSARKIPLTRVLTLLTVLFLVFLGCLPFGIOFLF--LMHVDREVLFCVHLVSLFLSA 262  
 DB 216 NTWASHSKXIVIMVITIIIFLIFAMPRVLYLYEYV-----SAFGNLHNISLFTST 269  
 QY 263 LNSSANPIYFVSGFRQNRONKLVLPALODASEV--DEGGC 306  
 DB 270 INSSANPIYFVSGSKKRRFRESIKVLTLPADQMPROQENG 315  
 RESULT 5  
 ID RTA RAT STANDARD; PRT; 343 AA.  
 AC P23749;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE Probable G protein-coupled receptor RTA.  
 GN RTA.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OC NCBI\_TaxId=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Aorta;  
 RX MEDLINE=90222168; PubMed=2109324;  
 RA Ross P.C., Figler R.A., Corjay M.H., Barber C.M., Adam N.,  
 RA Marcus D.R., Lynch K.R.;  
 RT "RTA, a candidate G protein-coupled receptor: cloning, sequencing,  
 RT and tissue distribution.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 87:3052-3056 (1990).  
 CC -1- FUNCTION: ORPHAN RECEPTOR.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: GUT, VAS DEFERENS, UTERUS, AND AORTA BUT ONLY  
 CC BARLEY DETECTABLE IN LIVER, KIDNEY, LUNG, AND SALIVARY GLAND. IN  
 CC THE BRAIN, RTA IS MARKEDLY ABUNDANT IN THE CEREBELLUM.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC MOST SIMILAR TO MAS.  
 CC -----  
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 CC -----  
 DR EMBL; M35297; AAA42087.1; --  
 DR EMBL; M35298; AAA42088.1; --  
 DR PIR; A35639; A35639.  
 DR InterPro; IPR000276; GPCR\_Rhodopen.  
 DR Pfam; PF00001; 7tm\_1; 1.

DR PROSTATE; P500237; G PROTEIN RECP F1.1;  
 DR PROSTATE; P500262; G-PROTEIN RECP F1.2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 44  
 FT TRANSMEM 45 66  
 FT DOMAIN 67 82  
 FT TRANSMEM 83 104  
 FT DOMAIN 105 123  
 FT TRANSMEM 124 144  
 FT DOMAIN 145 160  
 FT TRANSMEM 161 181  
 FT DOMAIN 182 198  
 FT TRANSMEM 199 220  
 FT DOMAIN 221 241  
 FT TRANSMEM 242 263  
 FT DOMAIN 264 273  
 FT TRANSMEM 274 294  
 FT DOMAIN 295 343  
 SQ SEQUENCE 343 AA; 38364 MW; E4630007770941F4 CRC64;  
 Query Match 25.2%; Score 418; DB 1; Length 343;  
 Best Local Similarity 35.0%; Pred. No. 4.7e-21; Indels 10; Gaps 6;  
 Matches 99; Conservative 57; Mismatches 117;  
 QY 36 IVSLVGLGNNAVVLMLGCMRRNRFSTIYILNLAADFLSGRLIYSLF--SFI-SIP 91  
 DB 53 LTLCLGVNGVGLVLMFPGFSIKRTPSYIFLHLSADGILYLSKAVIALNLNGTFLGSP 112  
 QY 92 HTISKILYPVMPESYFAGLSFSAVSTERCISVLPWYRCHPETHSAVVCVLLMALSL 151  
 DB 113 DYVRASRIYGLCTFPAGVSLTPAISIERCVSIFPMYWRPKLSAGVCALLMLLSF 172  
 QY 152 LRSILEMMLGFLFSGADSAWCQSDFTIVAMILFCVLCGSSVLVILRLICGSRKIP 210  
 DB 173 LVTSIHNYFCMFPGHBSGTCALNMDISGILFLFPCVLPCLATLHVECRARRQ 232  
 QY 211 LT-RLVYVLTLLTVLFLVFLGCLPFGIOFLF--LMHVDREVLFCVHLVSLFLSALNAP 269  
 DB 233 RSKALNHVLAIVSVFLVSSIVIGIDWFLF-WF---QIPAPPEVVTDLCTINSAXP 288  
 QY 270 IYFVFGSFRQNRONKLVLPALODASEVDEGGCULPEI 312  
 DB 289 IYFVLAGRDKSRILMEPLRVVFORALRDGAEPDAASTPNTV 331  
 RESULT 6  
 ID GP44 HUMAN STANDARD; PRT; 395 AA.  
 AC O94574; O94765;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Putative G protein-coupled receptor GPR44 (Chemoattractant receptor-  
 DE homologous molecule expressed on Th2 cells).  
 GN GPR44 OR CRTH2 OR DLIR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=99156852; PubMed=10036181;  
 RX Marchese A., Sawzadargo M., Nguyen T., Cheng R., Heng H.H., Nowak T.,  
 RA Im D.S., Lynch K.R., George S.R., O'dowd B.F.;  
 RT "Discovery of three novel orphan G-protein-coupled receptors.";  
 RL Genomics 56:12-21 (1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=99138803; PubMed=9973380;  
 RA Nagata K., Tanaka K., Ogawa K., Kemmotsu K., Imai T., Yoshie O.,  
 RA Abe H., Tada K., Nakamura M., Sugamura K., Takano S.;

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RT "Selective expression of a novel surface molecule by human Th2 cells
in vivo."
RL J. Immunol. 162:1278-1286(1999).
(3)
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Mettner A., Schroeder S.;
RT "Tissue expression and chromosomal organization of a novel G protein-
coupled receptor";
RL Submitted (Mar-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ORPHAN RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL; AF118265; AAD21055.1; ALT_INIT.
DR EMBL; AB008535; BA074518.1; -.
DR EMBL; AF144308; AAD34539.1; -.
DR Genbank; HGNC:4502; GPR44.
DR MIM; 604837; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00037; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 33
FT TRANSMEM 34 56
FT DOMAIN 57 67
FT TRANSMEM 68 89
FT DOMAIN 90 106
FT TRANSMEM 107 127
FT DOMAIN 128 146
FT TRANSMEM 147 168
FT DOMAIN 169 210
FT TRANSMEM 211 231
FT DOMAIN 232 247
FT TRANSMEM 248 269
FT DOMAIN 270 288
FT TRANSMEM 289 308
FT DOMAIN 309 395
FT CARBOHYD 4 4
FT CARBOHYD 25 25
FT DISULFID 104 182
FT CONFLICT 375 395
SQ
SEQUENCE 395 AA; 43239 MW; 9DBB53B2008C1D1 CRC64;
Query Match 16.8%; Score 279.5; DB 1; Length 395;
Best Local Similarity 27.7%; Pred. No. 6.8e-12;
Matches 84; Conservative 66; Mismatches 114; Indels 39; Gaps 11;
QY 36 IVSLVGLTGNAAVVMWMLQCRMRNRNFAFSIYIINLAAADFLFSGRLYSLSFSISPH--- 92
Db 41 LASLIGLVENGVLLEFVVGCRMRQVVTVTWVHLMSDLASASLPFTY--FLAVGHSWE 98
QY 93 ---ITSKLIYVMMFSYFAGLSFISAVSTERCLSYMWITRCRPHLSAVVCYLLMAL 149
Db 99 LGTFPCKLHSSIIFLNMPSAGFLLSAISLDRCLOVRVPMVQNHRTVAARHVCICVIMAL 158
QY 150 SLRSISLSEW-----MLGCF-----FESGAD-SAMQOT-----SDFTVAVLI 185
Db 159 AVLMTVPFVFRDRTISLRDGRIMCYVNVLLNPGDRDRTCNRSQALAAVSKFL-LAVLV 217
QY 186 FLCVVLGSSVLVLRILRCGRKIPRLRYVYITLITVLVFLLCGLPGIQFFELFLMWHD 245

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Db	218	PLA11	ASSHAAVSIKRLQHGRRP	GFFVRLVAAVNAFALCWGPHVFSLEBARAHN	275
Qy	246	--REVLEFCHVHLVSIPLSALNSSANPIIYFVFGSFRORONIKLVLQALADASEVD			302
Db	276	PGLRLPLVWRGLPEPVT	SLAFNFSVANPLVLYVTCRDMRLKRLRSJRTVLESVLVDSDSEIG		334
Qy	303	EGG	305		
Db	335	GAG	337		
RESULT 7					
GP44_MOUSE	ID	GP44_MOUSE	STANDARD:	PRT:	382 AA.
AC	Q92ZJ6:				
DT	30-MAY-2000	(Rel. 39, Created)			
DT	30-MAY-2000	(Rel. 39, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	Putative G protein-coupled receptor GPR44 (chemoattractant receptor-homologous molecule expressed on Th2 cells).				
CN	GN	GN	GN	GN	GN
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.				
OX	NCBI_Taxid=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=128/SvJ;				
EX	MEDLINE=99312318; PubMed=9931443;				
RA	Abe H., Takekita T., Nagata K., Arita T., Endo Y., Fujita T., Takayama H., Kubo M., Sugamura K.;				
RT	"Molecular cloning, chromosome mapping and characterization of the mouse CRT2 gene, a putative member of the leukocyte chemoattractant receptor family";				
RL	Gene 227:71-77(1999).				
CC	-1- FUNCTION: ORPHAN RECEPTOR.				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	-----				
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CC	-----				
CC	EMBL; AF054507; AAD13525.1; --				
DR	MGD; MGI:1330275; GPR44.				
DR	InterPro; IPR000276; GPCR_Rhodopsn.				
DR	Pfam; PF00001; 7tm_1, 1.				
DR	PRINTS; PR00237; GPCRHDODPSN.				
DR	PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.				
KW	PROSITE; PS02622; G-PROTEIN RECP_F1_2; 1.				
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.				
FT	DOMAIN	1	32	EXTRACELLULAR (POTENTIAL).	
FT	TRANSSEM	33	55	1 (POTENTIAL).	
FT	DOMAIN	56	66	CYTOPLASMIC (POTENTIAL).	
FT	TRANSSEM	67	88	2 (POTENTIAL).	
FT	DOMAIN	89	105	EXTRACELLULAR (POTENTIAL).	
FT	TRANSSEM	106	126	3 (POTENTIAL).	
FT	DOMAIN	127	145	CYTOPLASMIC (POTENTIAL).	
FT	TRANSSEM	146	167	4 (POTENTIAL).	
FT	DOMAIN	168	209	EXTRACELLULAR (POTENTIAL).	
FT	TRANSSEM	210	230	5 (POTENTIAL).	
FT	DOMAIN	231	246	CYTOPLASMIC (POTENTIAL).	
FT	TRANSSEM	247	268	6 (POTENTIAL).	
FT	DOMAIN	269	287	EXTRACELLULAR (POTENTIAL).	
FT	TRANSSEM	288	307	7 (POTENTIAL).	
FT	DOMAIN	308	357	CYTOPLASMIC (POTENTIAL).	
FT	CARBOHYD	21	21	N-LINKED (GLCNAC... ) (POTENTIAL).	
FT	CARBOHYD	21	21	N-LINKED (GLCNAC... ) (POTENTIAL).	

FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT DISULFID 103 181 POTENTIAL.  
 SQ SEQUENCE 382 AA; 42949 MW; 8CCB89893795B04 CRC64;  
 Query Match 15.8%; Score 262; DB 1; Length 382;  
 Best Local Similarity 25.1%; Pred. No. 9.3e-11; Mismatches 122; Indels 64; Gaps 14;  
 Matches 88; Conservative 76; Mismatches 122; Indels 64; Gaps 14;  
 1 MDPTISTDELTPINGTEETLCYKQTLSTLVTLCIVSLVGLTGNAAVLMILGCRMRNA 60  
 6 LKPLCPLEEMVQJPNHNSNSLRYIDHVS-ILHGLASLLGLVNGHLLFLVCGCRMQTV 64  
 61 FSTIILNAADEFLLSGRLYSLSLSTPH-----TSKILYPMMSYRGLSFLS 114  
 65 VTTVVLHLSLSDLLAASLPPFTY--FLAVGSHWELGTFCKLHSSVFLNMFASGFLLS 122  
 115 AVSTERCLSVLPIWYRCHRPHTLSAVYCVLMLSLSLSLFLE-----MLCG 162  
 123 AISDRCLQVYRPMQNRHTVAAHRYCLMLMLAVNTIPYVFPDTPRLDGRIMCY 182  
 163 FLF---SGAD-SAMQC-----TSDFITVAMLIPLCVLCSSVLILRILCGSKRIP 210  
 183 YNLLMNGPDRDTCYRQKALAVSKPL-LAFVPLAIL-ASSHVAVSILHHRGHO-- 238  
 211 LTRLVYTLVLV-FLICGLPFGIQLFLMIHVDREVLCHVHLVSIF----- 259  
 239 RTGRFRLVAIVAFVLCWGPYH-----FSLPARASHVTLTQLASRLGPF 287  
 260 ---LSANSSANPIYFVSGFRQRONKLVLRALODASEVDEGG 306  
 288 VTSIAFNSVNPILYVFTCPDMLYKLRSLRAVLESVLVEDS--DQSGG 335

RESULT 8  
 CML1 HUMAN STANDARD; PRT: 373 AA.  
 ID Q99768; Q99769; Q75748;  
 AC 15-0UL-1998 (Rel. 36, Created)  
 DT 15-0UN-2002 (Rel. 41, Last sequence update)  
 DT 15-0UN-2002 (Rel. 41, Last annotation update)  
 DE Chemokine receptor-like 1 (G-protein coupled receptor DEZ) (G protein-coupled receptor ChemR23).  
 DE CMTKRI or DEZ or CHEMR23.  
 GN Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OC NCBI\_Taxid:9606;  
 OX [1]  
 RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RP MEDLINE:97289630; PubMed:9144535;  
 RX Mettner A., Hermy G., Schinke B., Hermans-Borgmeyer I.;  
 RT "A novel G-protein-coupled receptor with homology to neuropeptide and chemotactant receptors expressed during bone development";  
 RL Biochem. Biophys. Res. Commun. 233:336-342 (1997).  
 [2]  
 RP SEQUENCE FROM N.A. (ISOFORM B).  
 RX MEDLINE:98264639; PubMed:9603476;  
 RA Samson M., Edinger A.L., Stordeur P., Rucker J., Verhaselt V.,  
 RA Sharoun M., Govaerts C., Mollereau C., Vassart G., Doms R.W.,  
 RA Parmentier M.;  
 RA "ChemR23, a putative chemotactant receptor, is expressed in monocyte-derived dendritic cells and macrophages and is a coreceptor for HIV and some primary HIV-1 strains";  
 RT Eur. J. Immunol. 28:1689-1700 (1998).  
 RL -1- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOTACTIC PEPTIDE RECEPTOR. MAY HAVE A FUNCTION IN BONE METABOLISM. ACTS AS A CORRECTOR FOR SEVERAL HIV STRAINS (SIIVAC316, SIIVAC339, SIIVAC342-2).  
 CC (92JG024-2).  
 CC SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, A (SHOWN HERE) AND B; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: PROMINENTLY EXPRESSED IN DEVELOPING OSSEOUS

CC AND CARTILAGINOUS TISSUE. ALSO FOUND IN ADULT PARATHYROID GLANDS.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING BONE DEVELOPMENT.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
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 CC  
 DR EMBL: U79526; AAC51258.1; -  
 DR EMBL: U79527; AAC51259.1; -  
 DR EMBL: Y14838; CA475112.1; -  
 DR Genbank; HGNC:12121; CMTKRI.  
 DR MIM; 602351; -  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm.1; 2.  
 DR PRINTS; PR00237; GPCR\_RHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECPT\_FL\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECPT\_FL\_2; 1.  
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Alternative splicing.  
 FT DOMAIN 1 41  
 FT TRANSSEM 42 64  
 FT DOMAIN 65 75  
 FT TRANSSEM 76 97  
 FT DOMAIN 98 114  
 FT TRANSSEM 115 135  
 FT DOMAIN 136 154  
 FT TRANSSEM 155 176  
 FT DOMAIN 177 224  
 FT TRANSSEM 225 245  
 FT DOMAIN 246 261  
 FT TRANSSEM 262 282  
 FT DOMAIN 283 300  
 FT TRANSSEM 301 320  
 FT DOMAIN 321 373  
 FT CARBOHYD 9  
 FT CARBOHYD 192 192  
 FT DISULFID 112 189  
 FT VARSPLIC 1 2  
 FT CONFLICT 248 248  
 SQ SEQUENCE 373 AA; 42322 MW; 5244B9738EC93834 CRC64;  
 Query Match 15.4%; Score 256.5; DB 1; Length 373;  
 Best Local Similarity 25.8%; Pred. No. 2.1e-10; Indels 75; Gaps 14;  
 Matches 90; Conservative 63; Mismatches 121; Indels 75; Gaps 14;  
 5 ISTDTELPINGTEETLCYKQTLSTLVTLCIVSLVGLTGNAAVLMILGCRMRNAFSIY 64  
 31 LSPLEAVTHI-----FLVVSIVYCPGLIANGVLIITAFKMKKTVNMW 77  
 65 ILNIAADFL--FLSGRLYSLSLSTPH--ISKILYVMMFSYFAGSLFSAVSTER 120  
 78 FLNLAIVADFLFNVLPHITVYAMDMYHVGTMCKISNELLHNNFVSFLITLISDR 137  
 121 CLSTVLMYWRCHRPHTLSAVYCVLMLSLSLFLE-----LEMMLCG-----LFS 166  
 138 CIVSLPVSQNSHNSVRLATVACVWVLAFLSSPBLVRDPAHNGKISCNNSLSLT 197  
 167 GADSAMCOTSDFITVAMLIPLCV--LCGSSVLIL-----RILCGSKRIPTRLVY 216  
 198 PGSSWPHGMDVGVSRHNVVTRFLGLPLVPLIIVACYLTYC--KIQNRNLAK 254  
 217 T-----ILLVLY-FLICGLPFGIQLFLMIHVDREVLCHVHLV-SIF-----L 260  
 255 TKKPKFIIVTIIIFFLCWCPY-----HTNLNLELHHTAMPSSVSLGIPLATL 304  
 261 SANSSANPIYFVSGFRQRONKLVLRALODASEVDEGGGLP 309  
 305 AANSCMNPILYVFMG-----QDFKKRVALFSLVNLASBEDTGHSSYP 348

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RESULT 9
FMT2_PANTR . STANDARD; PRT; 349 AA.
ID FMT2_PANTR .
AC P79243;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE N-formyl peptide receptor-like 2 receptor (Fragment).
GN PRL2.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=66421539; PubMed=8824156;
RA Alvarez V., Coto E., Sehen F., Gonzalez-Koces S., Lopez-Larrea C.;
RT "Molecular evolution of the N-formyl peptide and C5a receptors in
RL non-human primates."
CC Immunogenetics 44:446-452(1996).
CC -1- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES,
CC WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF
CC FMT2 TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS
CC RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A
CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X97743; CA66327.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS000237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 28 50 1 (POTENTIAL).
FT DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 62 83 2 (POTENTIAL).
FT DOMAIN 84 100 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 101 121 3 (POTENTIAL).
FT DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 141 162 4 (POTENTIAL).
FT DOMAIN 163 205 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 206 226 5 (POTENTIAL).
FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 243 266 6 (POTENTIAL).
FT DOMAIN 267 286 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 287 306 7 (POTENTIAL).
FT DOMAIN 307 349 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 98 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON TER 349 349 POTENTIAL.
SQ SEQUENCE 349 AA; 39611 MW; 88279F8C72915383 CRC64;

Query Match 15.4%; Score 256; DB 1; Length 349;
Best Local Similarity 27.6%; Pred. No. 2,1e-10;
Matches 92; Conservative 60; Mismatches 125; Indels 56; Gaps 13;
QY 14 PINGTEELCKKQKLSLVLTIVTIVSYV-----GLGNAYVYMLLCCRRRRAFSYIL 66
DB 8 PLNTEELV--PEPAGHTVIMFSLVHGVTVEGVGLNGVLVWAGFRMTRVNTICYL 65

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QY 67 NLAADFLFLSLGLIYLSL-----FISIPHTISKILYPMWESYFAGSLFSAVST 118
DB 66 NLADLDFSF-SALIPPRMYSVAMREKMPFCSF---LCKLVHWMDINDLFFSVYLITL 121
QY 119 ERLSLVLMPIWYCHRPHTLSAVVCVLAALS---LRSLLEN-----MLCGFL 164
DB 122 DRGICVLPMAQNNHRTMSLAKRWMTGLMTLITVLTPLEIFMTTTRTNGDTYCIFFNA 181
QY 165 FSGADSAMCOTSDPIFVAMLIPLCCSVLILIRIC-----GSRKIPLTRLY 215
DB 182 FWG-DTAVELNANFITMAKFFLIHLPIIGSMWSIITYCYGIARKHNMHMKSRPL 240
QY 216 VTLITLVFLPLGCLPFG-IGFPLFLMHVREVLF---CHVLVSI---FLSALNSA 267
DB 241 RVEAAVASFPCIFMPEYELIGLMAVWL---KEMLINGKYLITLVINPTSLAFNSCL 297
QY 268 NPITVEFVSFRORONKVLORALDQASE 300
DB 298 NPILVFMGNFQERLIRSLPSLERALTEVPD 330

RESULT 10
FMT2_GORGO . STANDARD; PRT; 340 AA.
ID FMT2_GORGO .
AC P79175;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE C5a anaphylatoxin chemotactic receptor (C5a-R) (Fragment).
GN C5R1 OR C5AR.
OS Gorilla gorilla gorilla (lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=66421539; PubMed=8824156;
RA Alvarez V., Coto E., Sehen F., Gonzalez-Koces S., Lopez-Larrea C.;
RT "Molecular evolution of the N-formyl peptide and C5a receptors in
RL non-human primates."
CC Immunogenetics 44:446-452(1996).
CC -1- FUNCTION: RECEPTOR FOR THE CHEMOTACTIC AND INFLAMMATORY PEPTIDE
CC ANAPHYLATOXIN C5A. THIS RECEPTOR STIMULATES CHEMOTAXIS, GRANULE
CC ENZYME RELEASE AND SUPEROXIDE ANION PRODUCTION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- PTM: SULFATION PLAYS A CRITICAL ROLE IN THE ASSOCIATION OF C5AR
CC WITH C5A, BUT NO SIGNIFICANT ROLE IN THE ABILITY OF THE RECEPTOR
CC TO TRANSDUCE A SIGNAL AND MOBILIZE CALCIUM IN RESPONSE TO A SMALL
CC PEPTIDE AGONIST (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; X97733; CA66317.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS000237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KW Chemotaxis.
FT NON TER 1 1
FT DOMAIN <1 30 1 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 31 53 1 (POTENTIAL).
FT DOMAIN 54 64 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 65 87 2 (POTENTIAL).
FT DOMAIN 88 103 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 104 125 3 (POTENTIAL).  
 FT DOMAIN 126 146 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 147 167 4 (POTENTIAL).  
 FT DOMAIN 168 193 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 194 219 5 (POTENTIAL).  
 FT DOMAIN 220 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 258 6 (POTENTIAL).  
 FT DOMAIN 259 275 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 276 296 7 (POTENTIAL).  
 FT DOMAIN 297 340 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 102 181 BY SIMILARITY.  
 FT MOD RES 4 4 SULFATION (BY SIMILARITY).  
 FT NON\_TER 7 7 SULFATION (BY SIMILARITY).  
 SO SEQUENCE 340 AA; 38235 MW; 214CFCE78A47B304 CRC64;

Query Match 15.2%; Score 252; DB 1; Length 340;  
 Best Local Similarity 26.6%; Pred. No. 3.8e-10;

Matches 89; Conservative 57; Mismatches 129; Indels 60; Gaps 10;

7 TLDTLPTINGBETLCYKQTLSTVLTCIVSLVGLGNVAVLMLGCMRRNAPSIIYL 66  
 12 TLDPN-ITVDKTSNTLRPDLAL-VIRAVFIVGVGNMVAWVTAPEAKRTINLWFL 69  
 67 NLAAADFL-FLSGRLIYLSLSTIPH-----TISKIIPYPMMSYFAGLSFSAVSTER 120  
 70 NLAAADFLSCIALPILFT--SIVQHHPFGGACRIPLSLILNMVASILLATISDR 127  
 121 CLSVLMPIMYRCHRTHTLSAVVCVLLMLSLRSLILEMNLGFLFSGADSAMCOTSPFIT 180  
 128 FLVVRKPIWCOFNRGAGLAMICAVAKGLALLTIPSL-----YRV 169  
 181 VAMLIPLCVLGLG-----SSVLILIRICGS--RKIPITRIYVITIL----- 220  
 170 VAEVEFPFVLGCVDYSHDKRERAVAVIRVLGLFWPLTLITCYTPTILRTMSRRATR 229  
 221 -----TVLVLGLCPFGIOFELFMITHVREVLFCVHLVSLFS--ALNSSAN 268  
 230 STRKLKVVAVVAVASFIFMLPYOVGTGIMMSFLEPSSPTFLLNKDSLCSVSAVINCCIN 289  
 269 PIIFYFVGSFPRONRONTLKLVLORALODASEYDE 303  
 290 PIIVYVAGGFGQRLAKSLPSILRNVLTEBSVRE 324

## RESULT 11

FML2 GORGO STANDARD; PRT; 349 AA.

AC P79178;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE FMLP-related receptor II (FMLP-R-II) (Fragment).  
 GN FPLP2.  
 OS Gorilla gorilla gorilla (lowland gorilla).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.  
 ON NCBI TaxID=9595;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96421539; PubMed=8824156;  
 RA Alvarez V., Coto E., Sehen F., Gonzalez-Koces S., Lopez-Iarrea C.;  
 RT "Molecular evolution of the N-formyl peptide and C5a receptors in  
 non-human primates.";  
 RL Immunogenetics 44:446-452(1996).  
 CC -I- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES,  
 WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF  
 FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS  
 RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A  
 PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.  
 CC SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----

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DR EMBL; X97742; CAA66326.1; -  
 DR InterPro; IPR00276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PROSITE; PS00237; G-PROTEIN RECP FL\_1; 1.  
 DR PROSITE; PS00262; G-PROTEIN RECP FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Chemotaxis.  
 FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 28 50 1 (POTENTIAL).  
 FT DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 62 83 2 (POTENTIAL).  
 FT DOMAIN 84 100 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 101 121 3 (POTENTIAL).  
 FT DOMAIN 122 140 4 (POTENTIAL).  
 FT TRANSMEM 141 162 5 (POTENTIAL).  
 FT DOMAIN 163 205 6 (POTENTIAL).  
 FT TRANSMEM 206 226 7 (POTENTIAL).  
 FT TRANSMEM 227 242 8 (POTENTIAL).  
 FT TRANSMEM 243 266 9 (POTENTIAL).  
 FT TRANSMEM 267 286 10 (POTENTIAL).  
 FT TRANSMEM 287 306 11 (POTENTIAL).  
 FT DOMAIN 307 349 12 (POTENTIAL).  
 FT CARBOHYD 4 4 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT DISULFID 98 176 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT NON\_TER 349 349 POTENTIAL.  
 SO SEQUENCE 349 AA; 39432 MW; C6ED77CFED023834 CRC64;

Query Match 15.2%; Score 252; DB 1; Length 349;  
 Best Local Similarity 27.6%; Pred. No. 3.9e-10;  
 Matches 92; Conservative 60; Mismatches 125; Indels 56; Gaps 13;

14 PINGTEETLCYKQTLSTVLTCIVSLV-----GLTGNVAVLMLGCMRRNAPSIIYL 66  
 8 PLNTEBEVL--PEPAGHTVIMFSLVHGVTFFGVGLGVAVIWAQFLMTRTVITCYL 65  
 67 NLAAADFLSGRLIYLSL-----FISIPHTISKIIPYPMMSYFAGLSFSAVST 118  
 66 NLAAADRSF-SALIFPMVSVAMREKMPGSGF--LCKLVHWIIDINLFSVYLITITL 121  
 119 ERCLSVLMPIMYRCHRTHTLSAVVCVLLMLSL--LRSLILEW-----MLCGFL 164  
 122 DRCLVLPMAQONHRMISAKRMVGMILITVLTPNPIFWTITSTNGDTYCIENFP 181  
 165 FSGADSAMCOTSPFITVAMLIPLCVLGGSSVLILIRILC-----GSKIPITRLY 215  
 182 FWG-DTAVERNLVITWAKVFLIHFIFGSMMSIITVCGYIIAKIRHNMIKSRPL 240  
 216 VTITLTVLVLGLPFG-IQFLFMITHVREVLF--CHVHVSF--FLSALNSSA 267  
 241 RVFAVAVASFICWPPYELGIIMAVL--KEMLNGKXIIIVLINPSSLAIFNSSL 297  
 268 NPIIFYFVGSFPRONRONTLKLVLORALODASE 300  
 298 NPIIVFLGNSFORRLRSLPFSRLALTEVPD 330

## RESULT 12

FML2 PONPY STANDARD; PRT; 349 AA.

AC P79237;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE N-formyl peptide receptor-like 2 receptor (fragment).  
 DE -----







```

RESULT 15.
CSAR MACMU STANDARD; PRT; 340 AA.
ID CSAR MACMU STANDARD; PRT; 340 AA.
AC P79188;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Csa anaphylatoxin chemotactic receptor (C5a-R) (Fragment).
GN CSAR1 OR CSAR.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9642153; PubMed=8824156;
RA Alvarez V., Coto E., Sehen F., Gonzalez-Koces S., Lopez-Larrea C.;
RT "Molecular evolution of the N-formyl peptide and C5a receptors in
RT non-human primates."
RL Immunogenetics 44:446-452(1996).
CC -1- FUNCTION: RECEPTOR FOR THE CHEMOTACTIC AND INFLAMMATORY PEPTIDE
CC ANAPHYLATOXIN C5A. THIS RECEPTOR STIMULATES CHEMOTAXIS, GRANULE
CC ENZYME RELEASE AND SUPEROXIDE ANION PRODUCTION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- PTM: SULFATION PLAYS A CRITICAL ROLE IN THE ASSOCIATION OF CSAR
CC WITH C5A, BUT NO SIGNIFICANT ROLE IN THE ABILITY OF THE RECEPTOR
CC TO TRANSDUCE A SIGNAL AND MOBILIZE CALCIUM IN RESPONSE TO A SMALL
CC PEPTIDE AGONIST (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X97731; CA66315.1; -
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KM Chemotaxis.
FT NON_TER 1 1
FT DOMAIN <1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 31 53 1 (POTENTIAL).
FT DOMAIN 54 64 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 65 87 2 (POTENTIAL).
FT DOMAIN 88 103 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 104 125 3 (POTENTIAL).
FT DOMAIN 126 146 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 147 167 4 (POTENTIAL).
FT DOMAIN 168 193 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 194 219 5 (POTENTIAL).
FT DOMAIN 220 235 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 236 258 6 (POTENTIAL).
FT DOMAIN 259 275 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 276 296 7 (POTENTIAL).
FT DOMAIN 297 >340 CYTOPLASMIC (POTENTIAL).
FT DISULFID 102 181 BY SIMILARITY.
FT MOD_RES 4 7 SULFATION (BY SIMILARITY).
FT MOD_RES 7 7 SULFATION (BY SIMILARITY).
FT NON_TER 340 340
SQ SEQUENCE 340 AA; 38274 MW; E11F7C73AB97FFB8 CRC64;
Query March 15.14; Score 250; DB 1; Length 340;
Best Local Similarity 26.24; Pred. No. 5.2e-10;
Matches 85; Conservative 66; Mismatches 135; Indels 38; Gaps 11;

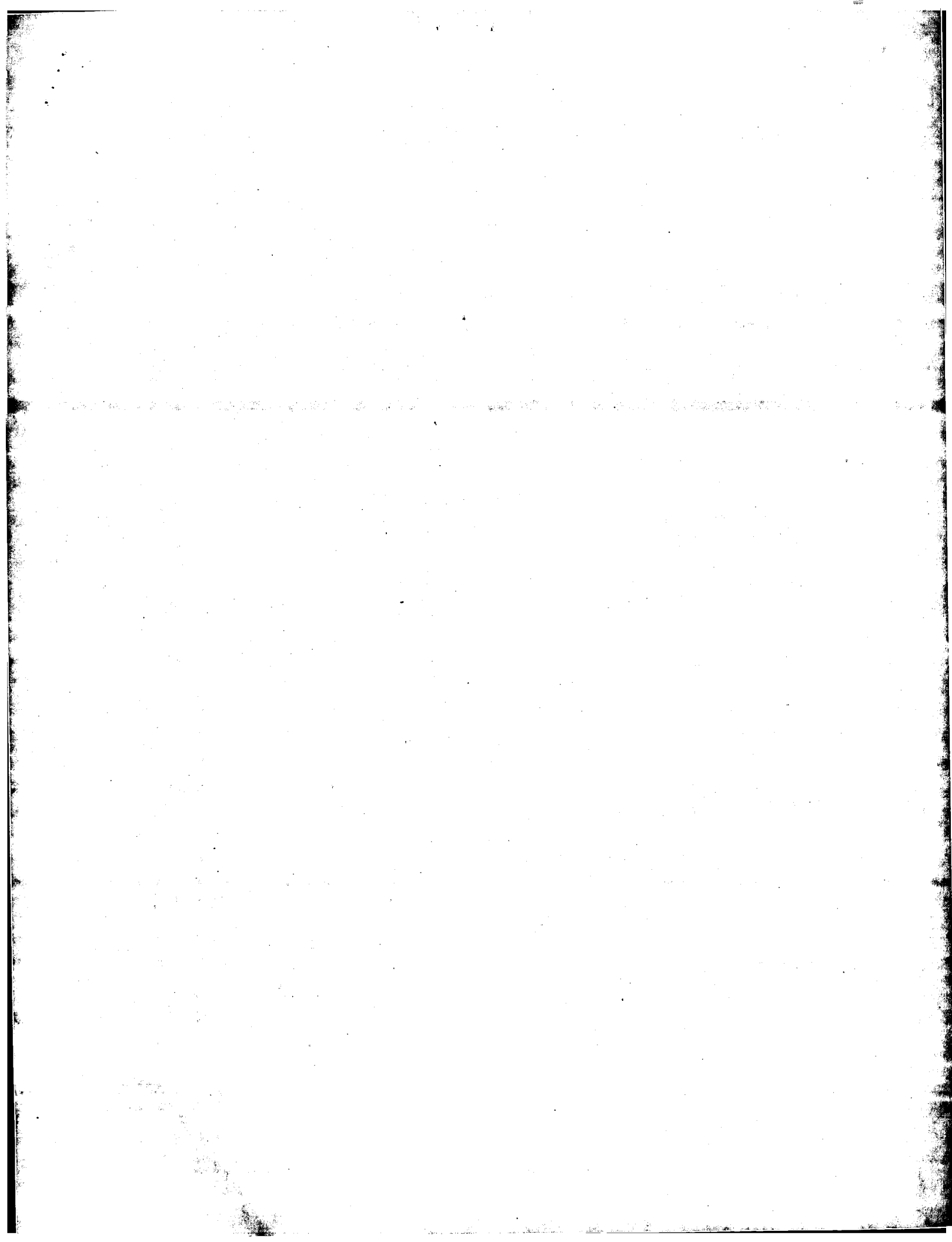
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QY 7 TLDTLPINGTEETLCYKOTLSLTVLTCTVSLVGLTGNVAVLMLGCRMRNNAFSIYL 66
Db 12 TLDPAN-TPVDKTSNTLRVPDIAL-VIFAVVFLVGLVRNALVWVNAFEAKRTINIMWL 69
QY 67 NLAADEL-FLSGRLIYSLFSISIPH-----TISKLYVMWMSYFAGLSFSAVSTER 120
Db 70 NLVADELFLSLAPILFT--SIQHHMPGGAACRLPSLILNMYASILLATTSADR 127
QY 121 CLSLWPIWYRCHRPPLNSAVCVLLMALSLRSILEM-----LCGFLPSG 167
Db 128 FLVENDPWQNRGAGLAWIACAVAMGLALLTIPSFLRVVREYFPPKVLG-VDHG 186
QY 168 ADSAKQTSPTIVAMLI-----FLCVLCSSVLVILGSKRIPLRLVITILT 221
Db 187 HDR--RREBAVAIARLVGFVWPLLTLMCYTFLRLTWSRRATSTKTLKVAVVAS 243
QY 222 VLVFLLCGLPFGIQLFELMIHYDREVLFGVHVLVSIFLS--ALNSANPIIYFVGSFR 279
Db 244 FFIFF--WLPQYTGMMMSFLRSPSPFLLLKTKDLSLCISFAYINCCINPIIYVAGQGF 300
QY 280 QRONRONLKIIVLQPALQDASEVDE 303
Db 301 QGRLKRSPLSLNVLNVLTEESMRE 324

```

Search completed: July 2, 2003, 19:21:01  
Job time: 12 secs



GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: July 2, 2003, 19:18:35 ; Search time 19 Seconds  
(without alignments)  
1629.225 Million cell updates/sec

Title: US-09-849-869A-16  
Perfect score: 1661  
Sequence: 1 MDPFTSLDLELFPINGTEE.....EGGGQLPEHLELSGRLEQ 322

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR 73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	484.5	29.2	324	1 TVRTAS	transforming prote
2	462	27.8	378	2 A39485	transforming prote
3	461.5	27.8	325	1 TVHUS	transforming prote
4	456.5	27.5	324	2 S51001	transforming prote
5	418	25.2	343	2 A35639	G protein-coupled
6	252	15.2	473	2 JC5835	anaphylatoxin C3a
7	251	15.1	353	2 C42009	FMPLP-related recep
8	250	15.1	350	1 A37963	complement C5a ana
9	248	14.9	351	2 B42009	FMPLP-related recep
10	243.5	14.7	369	2 A45291	somatostatin recep
11	242.5	14.6	355	2 A55733	G protein-coupled
12	241.5	14.5	369	2 D41795	somatostatin recep
13	236.5	14.2	346	2 S29248	somatostatin recep
14	236	14.2	364	2 A49542	N-formyl peptide c
15	230	13.8	371	2 JC5498	G protein-coupled
16	229	13.8	352	1 S27357	complement C5a ana
17	226	13.6	369	2 A23669	interleukin-8 rece
18	226	13.6	369	2 JC2083	somatostatin recep
19	225	13.5	352	2 A46520	N-formyl peptide r
20	224.5	13.5	355	2 J01231	interleukin-8 rece
21	224	13.5	388	2 JN0605	somatostatin recep
22	222.5	13.4	353	2 JC2492	G protein-coupled
23	221.5	13.3	363	2 A15940	somatostatin recep
24	221	13.3	371	2 JC5796	probable chemoattr
25	219.5	13.2	369	2 B41795	somatostatin recep
26	219.5	13.2	384	2 A47249	brain-specific som
27	218.5	13.2	333	2 I38974	G protein-coupled
28	218.5	13.2	351	1 A46525	complement C5a ana
29	218	13.1	380	2 S36143	kappa opioid recep

30	217	13.1	380	2 A48227	kappa opioid recep
31	216.5	13.0	384	2 JC4629	somatostatin recep
32	215	12.9	428	2 A44021	somatostatin recep
33	214.5	12.9	350	2 A42009	N-formyl peptide r
34	214	12.9	370	2 JC5549	hepatic P2Y5
35	214	12.9	380	2 JC2434	kappa opioid recep
36	213	12.8	428	2 S30508	probable G protein
37	212.5	12.8	355	2 JC5067	G protein-coupled
38	212	12.8	354	2 T09353	G protein-coupled
39	211.5	12.7	380	2 A55259	kappa opioid recep
40	211	12.7	391	2 A41795	somatostatin recep
41	211	12.7	391	2 C41795	somatostatin recep
42	211	12.7	391	2 A39297	somatostatin recep
43	210.5	12.7	380	2 JC2338	kappa opioid recep
44	209.5	12.6	333	2 I65989	G protein-coupled
45	207.5	12.5	418	2 A46226	somatostatin recep

## ALIGNMENTS

## RESULT 1

TVRTAS  
transforming protein mas - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Dec-1989 #sequence\_revision 31-Dec-1989 #text\_change 18-Jun-1999

C/Accession: A31816

R/Young, D.; O'Neill, K.; Jessell, T.; Wiegler, M.  
Proc. Natl. Acad. Sci. U.S.A. 85, 5339-5342, 1988

A/Title: Characterization of the rat mas oncogene and its high-level expression in the hi

A/Reference number: A31816; MIMD:88276953; PMID:2455902

A/Accession: A31816

A/Molecule type: mRNA

A/Residues: 1-324 <YOU>

A/Cross-references: GB:003823; NID:G205313; PIDN:AAA41573.1; PID:G205314

C/Genetics:

A/Gene: mas

C/Superfamily: mas transforming protein

C/Keywords: G protein-coupled receptor; transforming protein; transmembrane protein

F:31-47/Domain: transmembrane #status predicted <TM1>

F:72-88/Domain: transmembrane #status predicted <TM2>

F:149-165/Domain: transmembrane #status predicted <TM3>

F:185-204/Domain: transmembrane #status predicted <TM4>

F:225-243/Domain: transmembrane #status predicted <TM5>

Query Match 29.2%; Score 484.5; DB 1; Length 324;  
Best Local Similarity 39.2%; Pred. No. 1.1e-32;  
Matches 112; Conservative 61; Mismatches 86; Indels 27; Gaps 10;

QY	37	VSLVGLTGNVAVMLGCRMRRAFSIYILNLAADFLPLSGRLI----
DB	41	ISPLGEVENGILMLPFCFRMRNPFTVYITHLISALISLFCIFLISIDALDYELSSGH 100
QY	93	TISKILYPV-MMFSYFAGLSFSAVSTERCISLVPIMWRCHRPHTLSAVVCVLAALSL 151
DB	101	YITVITLSTVFLFGVNTGLYLFLAISVERCLSTLYIWRCHRPKQASAVCLLALNSC 160
QY	152	LRSILEMMLGCLFSGADSAMCQTS-----FTV-AMLIFLCVVLGSSVLRLILC 204
DB	161	LVTTMEYVMC--IDSGEESH--SQSDCAVILIFIALISFLVFPMLKV--SSTLVVKIRK 215
QY	205	GSKRKIPRLRYVITLTLVFLICGLPFGQPLF--LWTHVREVLFCVHVLVSTFLSA 262
DB	216	NTAASHSKLYIIVITLITLIFAMRMVLYLLVEYW-----STFGALHISLIFST 269
QY	263	LNSANPFIYFVGSRFRONRQNLVLQALQDADEV--DEGGG 306
DB	270	INSANPFIYFVGSSKKRFRSLKAVLTLRAKDMQPRRGNG 315

## RESULT 2

A39485  
transforming protein (mrz) - human

C:Species: Homo sapiens (man)  
 C:Date: 28-Feb-1992 #sequence\_revision 17-Apr-1993 #text\_change 16-Jul-1999  
 C:Accession: A39485  
 R:Monnot, C.; Weber, V.; Stinckre, J.; Bihoreau, C.; Teutsch, B.; Corvol, P.; Clauser, M.; Endocrinol. 5, 1477-1487, 1991  
 A:Title: Cloning and functional characterization of a novel, mas-related gene, modulating A:Reference number: A39485; MUID:92130997; PMID:1723144  
 A:Accession: A39485  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-378 <MON>  
 A:Cross-references: GB:S78653; NID:9244209; PIDN:AA21255.1; PID:9244210  
 C:Superfamily: mas transforming protein  
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 27.8%; Score 462; DB 2; Length 378;  
 Best Local Similarity 37.4%; Pred. No. 9e-31;  
 Matches 114; Conservative 56; Mismatches 101; Indels 34; Gaps 9;

QY 16 NGTEETL-----CYKOTLSLTVL---TCIVSLVGLTGNVAVMLLGCRRRNAAFSIYI 65  
 DB 54 NETETITHMOMMAVGOALPLNTIAPKAVLVSLCGVILNGTVFMLCCG-ATNPVWYI 112  
 QY 66 LNLAADEPLFSS---GRLIYLSFISIPHTISKIIPVMMFSYPAGLSFLSAVSTERC 121  
 DB 113 LHLVAAVDIYICCSAVGFLQVTLTYHGVVFPIEDFLAIIISPFSEVCLLVAISTERC 172  
 QY 122 LSLVMPWYRCHRPHTLSAVVVCVLLMALSLRLSILEMNLGFLPSGADSAMCQTSDF 178  
 DB 173 VCVLPPIWYRCHRPYTSNVCTILMGLPFCINIVKSLFLTY-----KHWVACVIF 224  
 QY 179 ITVAMLT--FLCVLTCGSSVLVLRILICGSKRIPLTRXYVTLTLVAVFLCGPFGIOF 236  
 DB 225 LKLSGLFPAIISLVWCVSSLTLRLFCSSQOQKATRYAVAVQISAPFLMALPLSVAP 284  
 QY 237 FLPLMIVHDEVLFCHVHLVSLFSLALNSANPIIYFVSGSFROKRNKILVLOALQ 296  
 DB 285 LI-----IDPRKFWYTSYLISLFL-INSSANPIIYFVSGSLRKRKLSRVLIIQRLLA 338  
 QY 297 DASEY 301  
 DB 339 DKPEV 343

RESULT 3  
 TVHNAS  
 transforming protein mas - human  
 C:Species: Homo sapiens (man)  
 C:Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 18-Jun-1999  
 C:Accession: A01375  
 R:Young, D.; Waitches, G.; Birchemier, C.; Pasano, O.; Wigler, M.  
 Cell 45, 711-719, 1986  
 A:Title: Isolation and characterization of a new cellular oncogene encoding a protein with A:Reference number: A01375; MUID:86218084; PMID:3708691  
 A:Accession: A01375  
 A:Molecule type: DNA  
 A:Residues: 1-325 <YOV>  
 A:Cross-references: GB:M13150; NID:9187388; PIDN:AAA36199.1; PID:9307158  
 C:Genetics:  
 A:Gene: GDB:MAS1  
 A:Cross-references: GDB:120166; OMIM:165180  
 A:Map position: 6q24-6q27  
 C:Superfamily: mas transforming protein  
 C:Keywords: G protein-coupled receptor; glycoprotein; proto-oncogene; transforming prote

Query Match 27.8%; Score 461.5; DB 1; Length 325;  
 Best Local Similarity 38.5%; Pred. No. 8.7e-31;  
 Matches 104; Conservative 59; Mismatches 92; Indels 15; Gaps 5;

QY 37 VSLVGLTGNVAVMLLGCRRRNAAFSIYIINLAADEPLFSGRLI---YSLISFISIPH 92  
 DB 42 ISVGVFENGIIILMFLCFRRNRNPFVYITHLSADISLFLCIFISIDYALDYELSSGH 101  
 QY 93 TISKILYPV-MMSYFAGLSFLSAVSTERCSTLMTLPIWYRCHRPHTLSAVVCTLMALSL 151  
 DB 102 YVTVLTVSLVFLPGYNTGYLTLAISVERLSVLYPIWYRCHRPKYQSAVLCALMALSC 161  
 QY 152 LRSILEMNLGFLPSGADSAMCQTSDFITVAMLIPLCV--VLGSSVLVLRILICSRKI 209  
 DB 162 LVTTMEYVWCIDDEESHSHNDCAVYIFPAISFLVFPPLMVLSSITLVKIRKNTWS 221  
 QY 210 PLTRLYVTLTLVAVFLCGLPFGIOFLE--LMIHDEVLFCHVHLVSLFSLALNSA 267  
 DB 222 HSKSLYIVIMVTLIIIFLFAMPRLLYLYEYW-----STFGNLIHISLFLSTINSSA 275  
 QY 268 NPITIFPVSGSFROKRNKILVLOALQD 297  
 DB 276 NPITIFPVSGSKKRFKSLKVLVTRAFKD 305

RESULT 4  
 transforming protein mas - mouse  
 N:Alternate names: mas proto-oncogene protein; probable G protein-coupled receptor mas  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 20-Apr-2001  
 C:Accession: S51001; I48647; S29619  
 R:Metzger, R.; Bader, M.; Ludwig, T.; Berberich, C.; Bunnemann, B.; Ganten, D.  
 FEBS Lett. 357, 27-32, 1995  
 A:Title: Expression of the mouse and rat mas proto-oncogene in the brain and peripheral A:Reference number: S51001; MUID:95094925; PMID:8001672  
 A:Accession: S51001  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-324 <MET>  
 A:Cross-references: EMBL:X67735  
 R:Metzger, R.; Bader, M.; Ludwig, T.; Berberich, C.; Bunnemann, B.; Ganten, D.  
 FEBS Lett. 357, 27-32, 1995  
 A:Title: Expression of the mouse and rat mas proto-oncogene in the brain and peripheral A:Reference number: I48647; MUID:95094925; PMID:8001672  
 A:Accession: I48647  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-87, 'I', 89-324 <RES>  
 A:Cross-references: EMBL:X67735; NID:953011; PIDN:CAA47964.1; PID:953012  
 C:Genetics:  
 A:Gene: mas  
 C:Superfamily: mas transforming protein  
 C:Keywords: G protein-coupled receptor; proto-oncogene; transmembrane protein

Query Match 27.5%; Score 456.5; DB 2; Length 324;  
 Best Local Similarity 38.1%; Pred. No. 2.2e-30;  
 Matches 109; Conservative 61; Mismatches 89; Indels 27; Gaps 10;

QY 37 VSLVGLTGNVAVMLLGCRRRNAAFSIYIINLAADEPLFSGRLI---YSLISFISIPH 92  
 DB 41 ISPIGFVENGILMLFLFRRNRNPFVYITHLSADISLFLCIFISTDYALDYELSSGH 100  
 QY 93 TISKILYPV-MMSYFAGLSFLSAVSTERCSTLMTLPIWYRCHRPHTLSAVVCTLMALSL 151  
 DB 101 HYTVTLTVSLVFLPGYNTGYLTLAISVERCLSVLYPIWYRCHRPKQSAFVCLALSC 160  
 QY 152 LRSILEMNLGFLPSGADSAMCQTSDFITV-AMLIPLCVVLCGSSVLVLRILIC 204  
 DB 161 LVTTMEYVWC-IDSGESH--SRSDCAVYIFPAISFLVFPPLMVLSS-ILVAVIRK 215  
 QY 205 GSRKIPTRLYVTLTLVAVFLCGLPFGIOFLE--LMIHDEVLFCHVHLVSLFLSA 262

```
D6      216 NTMAASHSKLIYIMTIIIFLIPAMPKRVLYLLYEIW-----SAGFNHNTSLLPST 269
Q7      263 LNSSANPIIIFYFGSPROQRONTKLVLQRLQDASEV--DEGGG 306
           :|:||||| ||||| :::: :||:|| | | | : - |||
Db       270 INSSANPFIIFYFGSSKKRFPRESLKVTULTRFKDEMOPPROEGNG 315
```

## RESULT 5

G:protein-coupled receptor RTA - rat  
C:Species: *Rattus norvegicus* (Norway rat)  
C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 16-Jul-1999  
C:Accession: A35639  
R:ROSS, P.C.; FIGHTER, R.A.; CORJAY, M.H.; BARBER, C.M.; ADAM, N.; HARCUS, D.R.; LYNCH, K.  
Proc. Natl. Acad. Sci. U.S.A. 87, 3052-3056, 1990  
A:Title: RTA, a candidate G protein-coupled receptor: cloning, sequencing, and tissue distribution  
A:Reference number: A35639; MUID:90222168; PMID:2109324  
A:Accession: A35639  
A:Molecule type: mRNA  
A:Residues: 1-343 <ROS>  
A:Cross-references: GB:M3297; NID:G206809; PID:AAA42087.1; PID:G206810; GB:M32098  
C:Superfamily: mas transforming protein  
C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein  
F:4/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match	25.2%	Score 418	DB 2	length 343
Best Local Similarity	35.0%	Pred. No. 3.6e-27		
Matches 99, Conservative	57	Mismatches 117	Indels 10	Gaps 6

QY 36 IVSLVGLTGNNAVVLWLLGCMRRNAFSIYILNLAAADPLFLSGRLIYSLL---SFL-SIP 91

Db 53 L L C L G L V G N G L V L W F F G F S I K R T P F S I Y F L H L S A D G I Y L F S K A V I A L I N M G T F L G S P 11

QY 92 HTISKILYPVMFSYPAGLSFLSAVSTERCLSVLPPIWYRCHPPTHLSAVVCVLLMALSL 15

Db 113 DYRRVSRIVGLCTFFAGVSLTPAISTIERCVSIFEPMMWYRRPKRI.SAGVCALWISF 177

152 1P81LENNI CGEI ESCGASAWCOTSEDTAVU TEL -CUNT CCCCCC VU1TDT CCCCCCVD 31

[illegible]

1/3 LVISHNIFCMFGHEASGTAQCNMDISLTGLTFPLCPMLVLPCLALILHVEGRARRQ 23

211 LT-RLVVTILLTVLVEFLLCGIPFGIOQFLEFLMWIHVDREVLCEHVHLVSIPLSALNSSANP 26

Db 233 RSAKLNHVLAIVSVFLVSSIYLGIIDWFLF-WVF---QIPAPFPEYVTDLCICINSSAKP 28

270 I I Y F V G S F R Q R O N K L V L Q R A L Q D A S E V D E G G L E E I 312

Db 289 IVYFLAGRDKSQRLMEPLRVVFQALRDGAEPGDAASTPNTV 331

## RESULT 6

anaphylatoxin C3a receptor - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 05-Mar-1998 #sequence Revision 13-Mar-1998 #text\_change 17-Mar-2000  
C/Accession: JCS835  
R/Fukunaka, Y.; Ember, J.A.; Hugli, T.E.  
Biochem. Biophys. Res. Commun. 242, 663-668, 1998  
A/Title: Cloning and characterization of rat C3a receptor: Differential expression of rat  
A/Reference number: JCS835; MUID:98125550; PMID:9464274  
A/Accession: JCS835  
A/Molecule type: mRNA  
A/Residues: 1-473 <FUK>  
A/Cross-references: GB:U86379; NID:g3105534; PIDN:AAC40071.1; PID:g2853279  
A/Experimental source: Brain  
A/Comment: This receptor plays a role in the central nervous systems.  
C/Superfamily: vertebrate rhodopsin  
C/Keywords: glycoprotein; phosphoprotein  
F:22-51/Domain: transmembrane #status predicted <TM1>  
F:58-83/Domain: transmembrane #status predicted <TM2>  
F:96-118/Domain: transmembrane #status predicted <TM3>  
F:138-160/Domain: transmembrane #status predicted <TM4>  
F:322-347/Domain: transmembrane #status predicted <TM5>

F\_367-392/Domain: #status predicted <TM6>  
F\_406-430/Domain: transmembrane #status predicted <TM7>  
F\_9\_201/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F\_360/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match	15.2%	Score 253	DB 2	Length 473
Best Local Similarity	20.5%	Pred. No. 2.4e-13		
Matches 95; Conservative	66	Mismatches 112	Indels 190	Gaps 14

7 TIDTELTPINGTEENTI.CYKOTI.SI.TVI.TCTVSI.VGI.TGNAYVI.WI.I.GCRMPRNPASTYII. 66

[illegible]

02 IADINSIDEN--SKFELAFQDIASMLTSDLCDDPGNSGZLVEMVAGVATMKRI VNI VWFL

BU

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67 NLAADF-----LFLSGRLIYSLLSFISIPHTISKILYPVMNMFSYFAGLSPLS 11
::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY

```

Db 63 HTLTADFLCCLSLPFSVAHLILRGHPYGLF-----LCKLIPSVIILNMFASVELLT 11

115 AVSTERCLSVLPPIWYRCHPHTLSAVCVLLMALSL-----RSIL---EWMLCGF 16 QY

Db 115 A I S L D R C L M H K P I M C N H R S V R T A F A V C G C W M V T F W M C I P F V F Y R D L L W D D Y S Y C G Y 17

QY 164 LFSG-----ADSAMCQTS----- 17

Db 175 NEDSSRAYDYWDYMNSHLPEINPPDNSTGVHDPRTAPSSSVPARDLMTATLALOSCTEH 23

177 ----- 177

[illegible]

235 TSPEDFSSQDSASQDPHIGSKPTVLIALIPGCFVVEDHKSNITLNGAFLSAHTEPSTLA 29

Qy 1.77 -----DF-----ITVAMLI-----FLCVLGGSSLVLLIRI 20

db 295 SSSPLAHDFPDDYFDQLMYGNHAWTPQVAITISRLVGVLPFFIMITCYSLSIVFRM-- 35

QY 203 LCGSRKIPTR-----LYVTILLTVLVFLCGLPFGIOFFFLMIHVD--REVLGCHVH 25

Db 353 ----RKTNLTCSRNKTLRVAVAV-VTVFVFCWIPYHIVGILVITDQESALREVLPWDH 400

255 LVSIFLSANSSANPIYEFVGSFRORONBOKLVIORALOD 297

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: ||:: || | : | : :: ||:: | : | :
408 M-STIASANSCENBELVALLCKDEPKKAPQSVYCTI.PAAEFT 449

```

RESIST

C42009  
FMLP-related receptor 2 - human  
N:Alternate names: FMLP-related receptor 1; probable chemotactic receptor FPRH2  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 26-Aug-1999  
C:Accession: C42009  
R:Bao, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.  
Genomics 13, 437-440, 1992  
A:Title: Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR),  
A:Reference number: A42009; MUID:92307661; PMID:1612600  
A:Accession: C42009  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-353 <BAO>  
A:Cross-references: GB:M76673; NID:G182668; PID:G182669  
C:Comment: This fMet-Leu-Phe receptor homolog, whose ligand is not yet known, appears not  
C:Genetics:  
A:Gene: GDB: FPR12  
A:Cross-references: GDB:128855; OMIM:136539  
A:Map position: 19q13.3-19q13.4  
A:Introns: #status absent  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 15.1%; Score 251; DB 2; Length 353;  
Best Local Similarity 27.0%; Pred. No. 2,2e-13;  
Matches 90; Conservative 61; Mismatches 126; Indels 56; Gaps 13;

14 PINGTEETLYCKQTLSTLVLTCTIVSLV--GLTGNAAVLMMLGCRMRRNAFSIYIL 66.

Db 8 PLNTEBEVL--PEBAGHTVLMISLVLVGVTFVGVGLNGVLVWVAGFMRTRVNTICV 65  
 Qy 67 NLAADFLFLSGRLIYSL-----FISIPHTIKILPYVMFSGFAGLSFSAVST 118  
 Db 66 NLAADSLF--SAILPFMVSVAMREKPFASF--LCKLVHWMIDNLFVSVLITLIAL 121  
 Qy 119 ERLSLVMPWYRCHRPTHLSAVVCVLLMALST--LRSLIEW-----MLCGFL 164  
 Db 122 DRICICVHPAWAKHRTMSLAKRVTMTGLMTFTVLTLPNFIPTWTITSTNGDYCIENFA 181  
 Qy 165 FSGGDSAMCQTSDFITVAMLIPLCVLVCSSVLVLIILC-----GSRKIPLTRLY 215  
 Db 182 FWG-DTAVERLVNTVTAKEFLILHPIITGVPEMSITTCYGIIAKHNNHMKSRPL 240  
 Qy 216 VTILTLTVLFLDGLPFG-IQFPLFLMIVHDEVLF--CHVHLVSI-----FLSALNSA 267  
 Db 241 RVFAAVASFFICMFPFELLIGLMAVWL--KEMLVNGKXKIIIVLINPTSLAFNSCL 297  
 Qy 268 NPITVFGVSFRQRONKMLVIGRALQDASE 300  
 Db 298 NPILVFGWGRNFORLIRSLPTSLERALTVEVD 330

## RESULT 8

complement C5a anaphylatoxin receptor - human

C.Species: Homo sapiens (man)

C.Date: 22-Jan-1993 #sequence revision 14-Feb-1997 #text\_change 21-Jul-2000

C.Accession: A37963; S13646; I52417; S30518

R.Boulay, F.; Merry, L.; Tardif, M.; Bouchon, L.; Vignais, P.

Biochemistry 30, 2993-2999, 1991

A>Title: Expression cloning of a receptor for C5a anaphylatoxin on differentiated HL-60

A.Reference number: A37963; PMID:2007135

A.Accession: A37963

A.Molecule type: mRNA

A.Residues: 1-350 <BOU>

A.Cross-references: GB:J05327; NID:G179699; PID:NAA62831.1; PID:G179700

R.Gerard, N.P.; Gerard, C.

Nature 349, 614-617, 1991

A>Title: The chemotactic receptor for human C5a anaphylatoxin.

A.Reference number: S13646; PMID:91156029; PMID:1847994

A.Accession: S13646

A.Molecule type: mRNA

A.Residues: 1-350 <GER>

A.Cross-references: EMBL:X58674; NID:G29566; PID:CB37830.1; PID:G4467832

R.Gerard, N.P.; Bao, L.; Xiao-Ping, H.; Eddy, R.L.

Biochemistry 32, 1243-1250, 1993

A>Title: Human chemotaxis receptor genes cluster at 19q13.3-13.4. Characterization of th

A.Reference number: I52417; PMID:93192225; PMID:8383526

A.Accession: I52417

A.Status: translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-3 <RES>

A.Cross-references: GB:S56556; GB:S56557; NID:G298577; NID:G298578

C.Genetics:

A.Gene: GDB:CSRI, CSA, CSAR

A.Cross-references: GDB:12886; OMIM:113995

A.Map position: 19q13.3-19q13.4

A.Introns: 1/3

A.Note: the list of introns may be incomplete

C.Function: mediates the inflammatory and chemotactic responses of polymorphonuclear

n

C.Superfamily: vertebrate rhodopsin

C.Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polymor

F:1-37/Domain: extracellular #status predicted <EX1>

F:38-61/Domain: transmembrane #status predicted <TM1>

F:62-71/Domain: intracellular #status predicted <TM2>

F:72-94/Domain: transmembrane #status predicted <TM2>

F:95-110/Domain: extracellular #status predicted <EX2>

F:111-132/Domain: transmembrane #status predicted <TM3>

F:133-149/Domain: intracellular #status predicted <IN2>

F:150-174/Domain: transmembrane #status predicted <TM4>

F:175-206/Domain: extracellular #status predicted <EX3>  
 F:207-227/Domain: transmembrane #status predicted <TM5>  
 F:228-242/Domain: intracellular #status predicted <IN3>  
 F:243-264/Domain: transmembrane #status predicted <EX6>  
 F:265-283/Domain: extracellular #status predicted <EX4>  
 F:284-307/Domain: transmembrane #status predicted <TM7>  
 F:308-350/Domain: intracellular #status predicted <IN4>  
 F:3/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.1%; Score 250; DB 1; Length 350;

Best Local Similarity 26.6%; Pred. No. 2.6e-13;

Matches 89; Conservative 56; Mismatches 130; Indels 60; Gaps 10;

Qy 7 TUDTELPNGHEELCKYQQTSLTVLCIYSLVGLTGNVAVMLGCRMRNPSIYL 66  
 Db 19 TUDTLN-TPVDKTSNLRPDDIAL-VIRAVFLVGLGNALVWVTAPEAKRTIAWFL 76  
 Qy 67 NLAADFL-FLSGRLIYSLFISIPH-----TSKILYPVMFSGFAGLSFSAVST 120  
 Db 77 NLAADFLSLALPILFT--SIVGHHPFGGACSIPLSLILNMVASILLATISADR 134  
 Qy 121 CLSVLMPWYRCHRPTHLSAVVCVLLMALSLRSLIEWMLCGFLFSGGDSAMCQTSDFIT 180  
 Db 135 FLIVFEPWQONFRGAGLAMIACAAMGLALLTIPSFV-----YRV 176  
 Qy 181 VAMLIPLCVLGC-----SSVLIPLRILCGS--RKIPLTRLYVTL----- 220  
 Db 177 VREVEYPPKVLGVSHDKREBAVAIRVAVGLFPLTLITICYFILLTWGRRA 236  
 Qy 221 -----TVLFLDGLPFGIQFPLFLMIVHDEVLFCHVHLVSIPLS--ALNSAN 268  
 Db 237 STKTLKVVAVVAFPIFPLPVQVTGIMMSFPFLINKLDSLCVSPAYINCIN 296  
 Qy 269 PIIVFVGVSFRQRONKMLVIGRALQDASEVD 303  
 Db 297 PIIVVAGGFGGRKRLKSLPSLRNLTESVRE 331

## RESULT 9

FMPL-related receptor 1 - human

N.Alternate names: FMPL receptor homolog FPR2, formyl peptide receptor like-1; probable

C.Species: Homo sapiens (man)

C.Date: 30-Sep-1993 #sequence revision 14-Jul-1995 #text\_change 21-Jul-2000

C.Accession: B42009; J01258; J01521; A42492; I54751; S21581

R.Bao, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.

Genomics 13, 437-440, 1992

A>Title: Mapping of genes for the human C5a receptor (C5AR), human FMPL receptor (FPR),

A.Reference number: A42009; PMID:92307681; PMID:1612600

A.Accession: B42009

A.Status: nucleic acid sequence not shown

A.Molecule type: DNA

A.Residues: 1-263, 'A', 265-338, 'C', 340-351 <BAO>

A.Cross-references: GB:M76672

A.Note: authors translated the codons GTG for residue 15 as GIV, TCT for residue 19 as TI

R.Perez, H.D.; Holmes, R.; Kelly, E.; McClary, J.; Andrews, W.H.

Gene 118, 303-304, 1992

A>Title: Cloning of a cDNA encoding a receptor related to the formyl peptide receptor of

A.Reference number: J01258; PMID:92380523; PMID:1511907

A.Accession: J01258

A.Status: nucleic acid sequence not shown

A.Molecule type: mRNA

A.Residues: 1-351 <PER>

A.Cross-references: EMBL:X63819; NID:G31460; PID:G31461

A.Experimental source: bone marrow mRNA

R.Ye, R.D.; Cavanagh, S.L.; Quehenberger, O.; Prossnitz, E.R.; Cochrane, C.G.

Biochem. Biophys. Res. Commun. 184, 582-589, 1992

A>Title: Isolation of a cDNA that encodes a novel granulocyte N-formyl peptide receptor

A.Reference number: J01521; PMID:92246937; PMID:11374236

A.Accession: J01521

A.Molecule type: mRNA

A.Residues: 1-351 <YE2>

A.Cross-references: GB:M88107; NID:G189862; PID:G189863



A:Experimental source: granulocytes  
 A:Note: formyl peptide-stimulated calcium mobilization comparable to that of the formyl  
 R:Murphy, P.M.; O'Connell, T.; Kenney, R.T.; Tiffany, H.L.; Mcdermott, D.; Franke, U.  
 J. Biol. Chem. 267, 7637-7643, 1992  
 A:Title: A structural homologue of the N-formyl peptide receptor. Characterization and c  
 A:Reference number: A42492; MUID:92218423; PMID:1373134  
 A:Accession: A42492  
 A:Molecule type: mRNA  
 A:Residues: 1-351 <MR>  
 A:Cross-references: GB:M4562; NID:g182741; PIDN:AAA52473.1; PID:g182742  
 A:Note: sequence extracted from NCBI backbone (NCBI:94159, NCBI:94160)  
 R:Nomura, H.; Nielsen, B.W.; Matsushima, K.  
 Int. Immunol. 5, 1239-1249, 1993  
 A:Title: Molecular cloning of cDNA encoding a LD78 receptor and putative leukocyte chem  
 A:Reference number: 154751; MUID:94092629; PMID:7505609  
 A:Accession: 154751  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-351 <RS>  
 A:Cross-references: GB:D10922; NID:g219864; PIDN:BAA01720.1; PID:g219865  
 C:Comment: This G-protein coupled receptor, homologous to the N-formyl peptide receptor  
 differentiated myeloid cells and is probably a chemotactic receptor for some other ligand  
 C:Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane protein  
 F:27-53/Domain: transmembrane #status predicted <TM1>  
 F:59-83/Domain: transmembrane #status predicted <TM2>  
 F:100-121/Domain: transmembrane #status predicted <TM3>  
 F:145-169/Domain: transmembrane #status predicted <TM4>  
 F:206-226/Domain: transmembrane #status predicted <TM5>  
 F:242-266/Domain: transmembrane #status predicted <TM6>  
 F:282-307/Domain: transmembrane #status predicted <TM7>  
 F:4/Binding site: carbonylate (Asn) (covalent) #status predicted  
 F:98-176/Disulfide bonds: #status predicted  
 Query Match 14.9%; Score 248; DB 2; Length 351;  
 Best Local Similarity 27.4%; Pred. No. 3.9e-13;  
 Matches 92; Conservative 61; Mismatches 121; Indels 62; Gaps 16;  
 QY 13 TPINGEETLCYK-----QTLSLVLTCTVSLVGLTGNAAVVMILGCRMRRAFSIYI 65  
 DB 7 TPLNBYEY-VSYEAGYTVIRILPLVVG-VTFVLGVLGGLVWAGFRTTRVTITICY 64  
 QY 66 LNTLAADFLPSGR--LIYSLSPISIPH--TISKILPYVMFVSFAGLSLAVSTERC 121  
 DB 65 LNTLAADFSFATLPLFLIVSWAGKMPFGWFLCKLHIIVDINLFGSVFLGFIADRC 124  
 QY 122 LSVLMPITWYCHRRTHLSAVVVCVLLMLSLRSLLEML-----CGFLFSGAD 169  
 DB 125 ICVHPHWAQNHKRVISLAKMVIQVPMILALVLTLPVFLFTVTTPNGDTYCTFNF---- 180  
 QY 170 SAMQTSQSD-----FTVAMLIPLCVLGGSSLVLLIRILC-----GSRKPLT 212  
 DB 181 ASMGCTEERLKVAILMTLARGIRFYI---GFLSPMSIYALICGLIAAKIHKKMKIKSS 237  
 QY 213 RLVTIILTVLVFLCGLPFGIOFPL-FLMTHDREVLFCVH-VLSIF-----LSALN 264  
 DB 238 RPLRLVLAIVASFPICWFFPOLVALLGTVMV---KEMLFQGYKIIDIIVNPSTSLAFN 294  
 QY 265 SSANPIYFFVG-SFRORONRNLKVLQRLQDAS 299  
 DB 295 SCLNPMILYVVGDFRRL-IHSLPTSLERALSDDS 329  
 RESULT 10  
 A45291  
 somatostatin receptor, somatostatin release-inhibiting factor receptor, SRIF receptor -  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 25-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jul-2000

C:Accession: A45291  
 R:Kluxen, F.W.; Bruns, C.; Lubbert, H.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 4618-4622, 1992  
 A:Title: Expression cloning of a rat brain somatostatin receptor cDNA.  
 A:Reference number: A45291; MUID:92262491; PMID:1374909  
 A:Accession: A45291  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-369 <KL>  
 A:Cross-references: GB:M93273; NID:g207026; PIDN:AAA42165.1; PID:g207027  
 A:Note: sequence extracted from NCBI backbone (NCBI:102315, NCBI:102316)  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G protein-coupled receptor; transmembrane protein  
 Query Match 14.7%; Score 243.5; DB 2; Length 369;  
 Best Local Similarity 27.6%; Pred. No. 9.5e-13;  
 Matches 96; Conservative 57; Mismatches 126; Indels 69; Gaps 13;  
 QY 3 PTISTDTELPINGEBETLCYKQTSIYVLTCTI---VSLVGLTGNAAVVM-LLGCRMR 58  
 DB 16 PSPFDLNGSLGPNNGNSQTEPYDMTSMNVLTFYFVVCVGLCGNTLVILRYAKMK 75  
 QY 59 NAFSIYTLNLAADFLPSGRILYSLSPISIPH-----TISKILPYVMFVSFAGLSFL 113  
 DB 76 TITNITILNLAIDELFMIG--LPFLAMQVALVHMFGRKICRVWMTVDGINDFTSIFCL 133  
 QY 114 SAVSTERCLSVLMPWYCHRPHTLSAVVVCVLLMLSLRSLLEML----- 160  
 DB 134 TWMSIRYLAIVHPISAKRRRRTAKMINIVAWGSL-LVLPIMIVAGLRNQGRSS 192  
 QY 161 CGFLFSGAGSAMQOTSDFTVAMLIPLCV---VLGSSVLVLR-----ILGSRKPLT 212  
 DB 193 CTINWPGESGAW--YTGFIITAFILGPLVPLTILCYFTIILKVGSSGIRGSSRKKS 250  
 QY 213 RLVT--ILITVLVFLCGLPFGIOFPLMTHDREVLFCVHLS----- 257  
 DB 251 EKVVTMNSIVAVVIFCMLP----FYIF-----NVSSVSAISPPALKMP 294  
 QY 258 ---IFLSALNSANPIYFFVGSFRORONRNLKVLQRLQDASEVD 302  
 DB 295 DFLVILTVANSCANPILYAFSLDNPFKSFQMYCLVKVSGAEDGERSD 342  
 RESULT 11  
 A55733  
 G protein-coupled receptor GPR1 - human  
 C:Species: Homo sapiens (man)  
 C:Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 21-Jul-2000  
 C:Accession: A55733  
 R:Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H.H.Q.; Tsui, L.  
 Genomics 23, 609-618, 1994  
 A:Title: Cloning of human genes encoding novel G protein-coupled receptors.  
 A:Reference number: A55733; MUID:95154831; PMID:7851889  
 A:Accession: A55733  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1335 <MAR>  
 A:Cross-references: GB:U13666; NID:g577412; PIDN:AAA64592.1; PID:g577413  
 C:Keywords: G protein-coupled receptor  
 Query Match 14.6%; Score 242.5; DB 2; Length 355;  
 Best Local Similarity 23.0%; Pred. No. 1.1e-12;  
 Matches 75; Conservative 59; Mismatches 97; Indels 95; Gaps 10;  
 QY 32 VLTCTVSVGLTGNAAVVM-LLGCRMRRAFSIYIINTLAADFLPSGRILYSLSPISIP 91  
 DB 43 VLYCLAFLVIGISGNALVIMFTGLKWKRTVITLPMILAIADFTL-----LFLP 91

QY HTSKILYPMWMEFY-----FAGLSPLSAVSTERCISLWPIWYRCH 133  
DB 92 LYSI---YVANNFHPFPGIWLCKANSTFQAOLNMFASVFLVLSLDRYHILHHPVLSHR 148  
QY 134 RPTHSANVCVLTWALSIL-----RSILEW 158  
DB 149 RFLNLSLIVIFILWLSLIGPALYPRDVEFNNHFLCYNNFQKHPDLILRHVLTW 208  
QY 159 M-LCGFLPSGADSAWCSOTDFITVAMILFICVVLCCGSSVLILRIICGSRKIPLTRLYV 216  
DB 209 VKFIIIGYLF-----PLLTMS-ICVLCILFKVKRRTVLIS-----SRHF 246  
QY 217 TILTLVFLVFLICGLPFGIQLFPLMIH---VDREVLFCVHLVSIPLSALNSANPIIYF 273  
DB 247 TILVAVVAFVVCWMPYHIFSTIWEILTIHNSYSHHWQAGIPL-STGLAFNLSCNPIILYV 305  
QY 274 FVGSFRORONRNLKVLQALQDAS 299  
DB 306 LSKKFGQARFRSSVAILKYLMEVS 331

## RESULT 12

D41795  
somatostatin receptor 2 - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 24-Nov-1999  
C:Accession: D41795; #56236  
R:Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.  
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992  
A:Title: Cloning and functional characterization of a family of human and mouse somatostatin receptor number: A41795; MUID:92108031; PMID:1346068  
A:Accession: D41795  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-369 <YAN>  
A:Cross-references: GB:M81832; NID:9201060; PIDN:AAA58256.1; PID:9201061  
R:Elliot, D.E.; Metwalli, A.; Blum, A.M.; Sandor, M.; Lynch, R.; Weinstein, J.V.  
J. Immunol. 153, 1180-1186, 1994  
A:Title: T lymphocyte isolated from the hepatic granulomas of schistosoma-infected mice  
A:Reference number: 156236; MUID:94300079; PMID:7913111  
A:Accession: 156236  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 99-309 <RES>  
A:Cross-references: GB:S71756; NID:9560631  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

Query Match 14.5%; Score 241.5; DB 2; Length 369;  
Best Local Similarity 27.7%; Pred. No. 1.4e-12;  
Matches 95; Conservative 56; Mismatches 123; Indels 69; Gaps 13;

QY 8 LDTELPIINGTEELCYKQTLSTVLTCT---VSLVGLTGNNAVLM-ILGCRMRNAPSI 63  
DB 21 LNSGLSPSGNSQTEPYDMTSMNAVLTIFYVAVCVGLCGMTLVYILIRYAKMKITIMI 80  
QY 64 YILNLAADFLFLSGRLIYSLSFISIPH-----TISKILYPMWMEFYFAGLSPLSAVST 118  
DB 81 YILNLAIDELFMLG--LPEFLAMQVALVHMPFGKACIRVMTVDGINDQFTSIFCLTWSI 138  
QY 119 ERLCLVIMPYWRCHPETHLSAVVCLWALSILRSILEMNL-----CGFLF 165  
DB 139 DRYLAVVHPFKSAKMRPRPTAKMINAVWCVSL-VILPIMLYAGLRSNQGRSSCTINW 197  
QY 166 SGADSAWCSOTDFITVAMILFICV---VLCGSSVLILR-----ILGSRKIPLTRLYT 217  
DB 198 PEGSGAM--YTGFIITAFILGFLVPLTITCLCYLFIILIKVSSGIRVSSKRSKSEKVT 255  
QY 218 --ILTLVFLVFLICGLPFGIQLFPLMIHVDREVLFCVHLVS-----IF 259  
DB 256 RMVSIIVAVFIFCWL---FYIF-----NVSSVAISPPALKGMFDFVVI 299  
QY 260 LSAIINSSANPIIYFVGSFRORONRNLKVLQALQDASEVD 302

DB 300 LTYANSCANPIIYAFILSDNFKKSFQVLCVLKVASGTEDEGERSD 342

## RESULT 13

S29248  
somatostatin receptor 2B - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-Nov-1999  
C:Accession: S29248  
R:Vanetti, M.; Kouda, M.; Wang, X.; Vogt, G.; Hoellt, V.  
FEBS Lett. 311, 290-294, 1992  
A:Title: Cloning and expression of a novel mouse somatostatin receptor (SSTR2B)  
A:Reference number: S29248; MUID:93012001; PMID:1397330  
A:Accession: S29248  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-346 <YAN>  
A:Cross-references: EMBL:X68951; NID:954197; PIDN:CAA48766.1; PID:954198  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 14.2%; Score 236.5; DB 2; Length 346;  
Best Local Similarity 27.9%; Pred. No. 3.4e-12;  
Matches 95; Conservative 56; Mismatches 121; Indels 69; Gaps 13;

QY 8 LDTELPIINGTEELCYKQTLSTVLTCT---VSLVGLTGNNAVLM-ILGCRMRNAPSI 63  
DB 21 LNSGLSPSGNSQTEPYDMTSMNAVLTIFYVAVCVGLCGMTLVYILIRYAKMKITIMI 80  
QY 64 YILNLAADFLFLSGRLIYSLSFISIPH-----TISKILYPMWMEFYFAGLSPLSAVST 118  
DB 81 YILNLAIDELFMLG--LPEFLAMQVALVHMPFGKACIRVMTVDGINDQFTSIFCLTWSI 138  
QY 119 ERLCLVIMPYWRCHPETHLSAVVCLWALSILRSILEMNL-----CGFLF 165  
DB 139 DRYLAVVHPFKSAKMRPRPTAKMINAVWCVSL-VILPIMLYAGLRSNQGRSSCTINW 197  
QY 166 SGADSAWCSOTDFITVAMILFICV---VLCGSSVLILR-----ILGSRKIPLTRLYT 217  
DB 198 PEGSGAM--YTGFIITAFILGFLVPLTITCLCYLFIILIKVSSGIRVSSKRSKSEKVT 255  
QY 218 --ILTLVFLVFLICGLPFGIQLFPLMIHVDREVLFCVHLVS-----IF 259  
DB 256 RMVSIIVAVFIFCWL---FYIF-----NVSSVAISPPALKGMFDFVVI 299  
QY 260 LSAIINSSANPIIYFVGSFRORONRNLKVLQALQDASE 300  
DB 300 LTYANSCANPIIYAFILSDNFKKSFQVLCVLKADNSQGA 340

## RESULT 14

A49542  
N-formyl peptide chemotactic receptor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 05-Nov-1999  
C:Accession: A49542  
R:Geo, J.L.; Murphy, P.M.  
J. Biol. Chem. 268, 25395-25401, 1993  
A:Title: Species and subtype variants of the N-formyl peptide chemotactic receptor reveal  
A:Reference number: A49542; MUID:94064602; PMID:8244972  
A:Accession: A49542  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-364 <GNO>  
A:Cross-references: GB:L22181; NID:9347396; PIDN:AAA16110.1; PID:9347397  
C:Genetics:  
A:Introns: #status absent  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: chemotaxis; transmembrane protein

Query Match 14.2%; Score 236; DB 2; Length 364;  
Best Local Similarity 24.8%; Pred. No. 3.9e-12;

Matches 84; Conservative 57; Mismatches 132; Indels 66; Gaps 13;

Search completed: July 2, 2003, 19:22:54  
Job time : 21 secs

```

Qy 32 VLVCIYSVLVTGNNAVVLMLGGRMRNNAFSYIYINLAAQFLFSGRLYSILSFSIP 91
   . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 39 LIRAVFVLGVGLNGVLIVWAGFPMKHVYTTISYINLADPCTFS-TLPRYIASPMGCG 97
   . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 92 H-----TISKILYPMVMSFYFAGLSFSLAVSTERCLSVMIPIWYCRHPHLSAVCVLL 146
   . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 98 HMFEGFMCFEITVVIDINLFGSVFLIALIDRCICVLHNVMAONHRYSLAKKVIIVP 157
   . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 147 WALSLRSILEMMLGCFELS-----GASAMACQSDS-----I 179
   . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 158 W-----ICAFLLTLPIIRLTTPVPSRSRGPKTKAC-TPDPSQWTKDVEGRKV 204
   . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 180 TVAMLIFLCV--LGGSSLVLLIRLIC-----GSRKIPLTRLYVTLITLVVLLC 228
   . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 205 AVMLTVVRGRIIRPIIGFSTPMGSLVAILCYGLITTKIHRGILKSSGPIRLVSFVVAAPFLIC 264
   . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 229 GLRPFGIQFLFLWIVHDREVLEFCHVILVSI-----LSALNLSANPIIYFVFG--SFEQRQ 282
   . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 265 WCFPGV-VALISPIQVRERLAKMTPEIYVIALKITSPLAFNISCUNPMLIYVMQDPFERL 323
   . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 283 NRONLKIYVQRL-QDASEVDGEGGOLPREILIELSGSL 320
   . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 324 -TSLPASTLERALTEDSAQTSIDGTNLGTNSGTSLENTL 361
   . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

## RESULT 15

G:protein-coupled receptor DE2 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-Jul-1997 #sequence revision 29-Aug-1997 #ext\_change 19-May-2000  
C:Accession: J05498  
R:Mathner, A.; Herney, G.; Schinke, B.; Hermans-Borgmeyer, I.  
Biochem. Biophys. Res. Commun. 233, 336-342, 1997  
A:Title: A novel G protein-coupled receptor with homology to neuropeptide and chemosensitive  
A:Reference number: J05498; MUID:97289630; PMID:9144535  
A:Contents: Brain  
A:Accession: J05498  
A:Contents: Brain  
A:Molecule type: mRNA  
A:Residues: 1-371 <MET>  
A:Cross-references: GB:U079525; NID:q1732346; PIDN:AAB53789.1; PID:q1732347  
C:Comment: This protein is involved in the bone metabolism.  
C:Superfamily: vertebrate rhodopsin  
F:110-187/Disulfide bonds: #status predicted

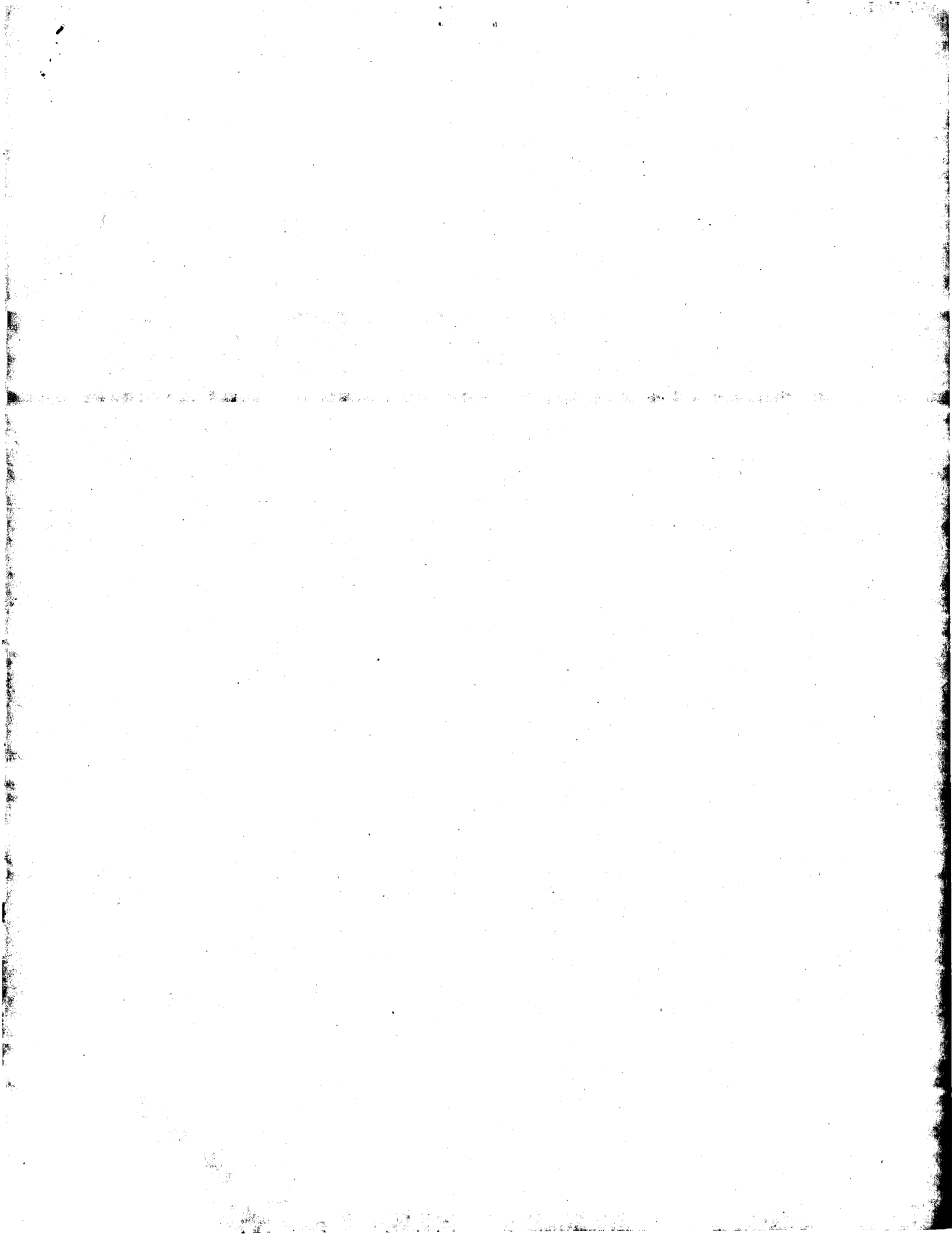
Query Match	Score	DB 2;	Length
13.8%	230;		371;

Best Local Similarity 25.2%; Pred No. 1 2e-11;  
Matches 82; Conservative 57; Mismatches 122; Indels 64; Gaps 12;

```

QY 30 LVAVTGCVSLVGLTGAUVAUMLTLCGRMRNAPSIIILNLAADFL---FLSGRLTYSLLS 86
Dd 41 LVVYSLVCTSLGSLGGLVIVATFCKKKTUVTTFVUVAADFLFNILPMHTTAAAD 100
QY 87 FISI-FHTISKILYFPMFSPFAGLSFLSASTERCISLWPIRYCHPHTLSAVVCYL 145
Dd 101 YHWFGRKAKCKISNPLLSHMYTSYFLLTVLISFDRCLISVLLPVMSONHSGIRLAYMTCSA 160
QY 146 LMAISLIRSLIEMWLCGLFPGSADSMACOTSPF---ITVAWLIFLC-----VY 190
Dd 161 VWVLA-----FLLSPSLVFRNTNANHOIKITCPNPFSLAPDSSPHNHSQV 208
QY 191 LCGSS---LVLLIRILCGSRKTP---LRRIVYT-----ILITLVV-F 225
Dd 209 STYSIRHVAATVTRFICGF-LIPVFLTACVLTIVFKLQRNRLAKNKKPFKIIITITITP 267
QY 226 LILGSLPFGIOQFLFLMIHVDRVLEFCHNVLVIFSLAINSSANPPIYFVWG-SFQRONR 284
Dd 268 FLICMRPHNTYLLLELHNHTAVPSSVSLSGIRPLATVAALNSCMNPILVYFMGHDRK--- 323
QY 285 QNLKVLQRLQDASEVDGCGQLP 309
Dd 324 --FKVALFSLNALASEDTGPPSSYP 346

```



GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: July 2, 2003, 19:13:29 ; Search time 72 Seconds  
(without alignments)  
595.926 Million cell updates/sec

Title: US-09-849-869A-16  
Sequence: 1 MDPRTSLDTRITNGTE.....EGGQLEPILLSGSLREQ 322  
Perfect score: 1661

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: A\_Geneseq\_101002:\*  
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
5: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
6: /SID2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
7: /SID2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
8: /SID2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
9: /SID2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
10: /SID2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
11: /SID2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
12: /SID2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
13: /SID2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /SID2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SID2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SID2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
17: /SID2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*  
18: /SID2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1661	100.0	322	22	AAE12794
2	1661	100.0	322	22	AAU04371
3	1661	100.0	322	22	AAU04371
4	1661	100.0	322	23	AAE21288
5	1661	100.0	322	23	AAE17074
6	1652	99.5	322	20	AAV30162
7	1624	97.8	322	20	AAV30161
8	1390	83.7	322	21	AAE14846
9	1383	83.3	322	21	AAV0761
10	1383	83.3	322	23	AAE21296

11	1383	83.3	337	23	AAU97598
12	1378	83.0	322	21	AAV90762
13	1373	82.7	322	20	AAV30159
14	1314	79.1	322	21	AAV87664
15	1313	79.0	322	20	AAV30160
16	1294	77.9	322	20	AAV30163
17	1294	77.9	322	21	AAV87663
18	1294	77.9	322	23	AAE21297
19	1287	77.5	322	20	AAU04376
20	1038.5	62.5	330	22	AAU62852
21	1038.5	62.5	330	22	AAU62852
22	1038.5	62.5	330	22	AAU62852
23	1038.5	62.5	330	22	AAU72910
24	1038.5	62.5	330	22	AAU72910
25	1038.5	62.5	330	23	AAE17289
26	1038.5	62.5	330	23	AAE17289
27	1038.5	62.5	330	23	AAE17289
28	1038.5	62.5	330	23	AAE17289
29	1038.5	62.5	330	23	AAE17289
30	1038.5	62.5	330	23	AAE17289
31	1033.5	62.2	330	23	AAU10590
32	1032	62.1	330	22	AAE09974
33	984	59.2	324	22	AAE09974
34	885	53.3	264	22	AAU78329
35	847	51.0	337	20	AAV30158
36	821	49.4	338	23	AAE21301
37	820	49.4	338	22	AAE173294
38	779	46.9	273	23	AAE21323
39	773.5	46.6	325	23	AAE08771
40	769.5	46.3	338	23	AAE21300
41	764.5	46.0	330	23	AAE21300
42	761.5	45.8	331	22	AAE12793
43	760.5	45.8	338	21	AAV7736
44	756.5	45.5	304	23	AAE21281
45	748.5	45.1	305	23	AAE21309

## ALIGNMENTS

RESULT 1	AAE12794	standard; Protein; 322 AA.
ID	AAE12794	
AC	AAE12794	
XX		
DT	15-JAN-2002	(first entry)
XX		
DE	Human G protein coupled receptor 1 (GPCR1).	
XX		
KW	Human, G protein coupled receptor; GPCR; purine receptor; vasodilation;	
KW	therapy; central nervous system disorder; sedative; antiinflammatory;	
KW	platelet aggregation; gastric secretion; apoptosis; neuroprotective;	
KW	inflammation; anticonvulsant; anticoagulant; bronchoconstrictor;	
KW	bronchodilator; vasoconstrictor.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200174902-A2.	
XX		
PD	11-OCT-2001.	
XX		
PF	02-APR-2001; 2001WO-EP03688.	
XX		
PR	04-APR-2000; 2000GB-0008252.	
XX		
PA	(JANC) JANSSEN PHARM NV.	
XX		
PI	Bender E, Buist A, Ercken M, Baggetman GLE, Jurzak M, Schoofs LAH;	
XX	Luyten WHM;	
XX	WPI; 2001-648551/74.	
DR	N-PDB; AAD20943.	

XX New G protein coupled receptor polypeptide, adenine binding G protein  
PT coupled receptor, useful in treatment of diseases in which pathology is  
PT associated with activity at purine receptors e.g. central nervous  
PT system disorders  
XX  
PS Claim 4, Fig 1, 81pp; English.  
XX  
CC The invention relates to G protein coupled receptor (adenine binding  
CC GPCR) and its corresponding nucleic acids. GPCR DNA is used to prepare  
CC medicaments for treating diseases in which pathology is associated with  
CC activity at purine receptors (especially mutation or downregulation of  
CC expression of native adenine binding GPCRs). GPCR DNA and its protein  
CC are used to treat central nervous system disorders (e.g. as sedatives,  
CC anticonvulsives, etc.), as stimulators of NO production by vascular  
CC endothelial cells, as inhibitors of platelet aggregation, gastric  
CC secretion or in diseases associated with apoptosis, vasodilation,  
CC bronchoconstriction or inflammation. They are useful to identify  
CC interacting compounds useful to treat these diseases. They are used to  
CC generate antibodies, useful to detect polypeptide (e.g. diagnostically),  
CC in polypeptide purification and therapeutically. GPCR DNA is also used  
CC to produce probes and primers, useful to detect/quantify polynucleotides  
CC (e.g. diagnostically or in tissue distribution studies) or to isolate  
CC similar sequences (e.g. from other species). The present sequence is  
CC human GPCR1 protein.  
CC  
XX  
SQ Sequence 322 AA;  
Query Match 100.0%; Score 1661; DB 22; Length 322;  
Best Local Similarity 100.0%; Pred. No. 4e-171;  
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPITSTLDTLPTINGTEETLCYKQTLSTLVLTCTIVSLVGTGNAVAVMLLGCGRMRNA 60  
DB 1 MDPITSTLDTLPTINGTEETLCYKQTLSTLVLTCTIVSLVGTGNAVAVMLLGCGRMRNA 60  
QY 61 FSIYILNLAADFLFLSGRLIYSLISFISIPHTISKILYPVMWFSYFAGLSFSAVSTER 120  
DB 61 FSIYILNLAADFLFLSGRLIYSLISFISIPHTISKILYPVMWFSYFAGLSFSAVSTER 120  
QY 121 CLSVLMPWYRCHRPHTLSAVVAVCVLLMALSLRSLLEWMLCGFLPSGADSAMCQTSDFIT 180  
DB 121 CLSVLMPWYRCHRPHTLSAVVAVCVLLMALSLRSLLEWMLCGFLPSGADSAMCQTSDFIT 180  
QY 181 VAMLIPLCVVLCGSSIVLLIRILCGSRKIPLTRLYVTITLVVFLVLCGLPGIOFPLFL 240  
DB 181 VAMLIPLCVVLCGSSIVLLIRILCGSRKIPLTRLYVTITLVVFLVLCGLPGIOFPLFL 240  
QY 241 WIHVREVLFCVHVLVSIPLSALNSSANPIIFVFGSFPQRONRNLKVLQRALQDASE 300  
DB 241 WIHVREVLFCVHVLVSIPLSALNSSANPIIFVFGSFPQRONRNLKVLQRALQDASE 300  
QY 301 VDEGGGQLPBEIILELGSRLAQ 322  
DB 301 VDEGGGQLPBEIILELGSRLAQ 322

RESULT 2  
AAU04371  
ID AAU04371 standard; Protein; 322 AA.  
XX  
AC AAU04371;  
XX  
DT 23-OCT-2001 (first entry)  
XX  
DE Human G-protein coupled receptor, hrUP17.  
XX  
KM Human; G-protein coupled receptor; GPCR; hrUP17; agonist;  
XX  
OS Inverse agonist; lung cancer.  
XX  
PN Homo sapiens.  
XX  
PN WO200136471-A2.

XX  
PD 25-MAY-2001.  
XX  
PF 16-NOV-2000; 2000MO-US31509.  
XX  
XX 17-NOV-1999; 99US-0166088.  
XX 17-NOV-1999; 99US-0166099.  
XX 17-NOV-1999; 99US-0166369.  
XX 23-DEC-1999; 99US-0171900.  
XX 23-DEC-1999; 99US-0171901.  
XX 23-DEC-1999; 99US-0171902.  
XX 11-FEB-2000; 2000US-0181749.  
XX 14-MAR-2000; 2000US-0189258.  
XX 14-MAR-2000; 2000US-0189259.  
XX 10-APR-2000; 2000US-0195898.  
XX 10-APR-2000; 2000US-0195899.  
XX 10-APR-2000; 2000US-0196078.  
XX 28-APR-2000; 2000US-0200419.  
XX 12-MAY-2000; 2000US-0203630.  
XX 12-JUN-2000; 2000US-0210741.  
XX 12-JUN-2000; 2000US-0210982.  
XX 21-AUG-2000; 2000US-0226760.  
XX 26-SEP-2000; 2000US-0235418.  
XX 26-SEP-2000; 2000US-0235779.  
XX 20-OCT-2000; 2000US-0242332.  
XX 20-OCT-2000; 2000US-0242343.  
XX  
XX (AREN-) ARENA PHARM INC.  
XX  
XX Chen R, Dang HT, Lowitz KP;  
XX  
XX WPI: 2001-355616/37.  
XX  
XX N-PSDB: AAS07944.  
XX  
XX Endogenous and non-endogenous versions of human G-protein coupled  
XX receptors for direct identification of candidate compounds as agonists,  
XX inverse agonists or partial agonists for use as therapeutic agents -  
XX  
XX Claim 37, Page 107; 160pp; English.  
XX  
XX The sequence represents a human G-protein coupled receptor (GPCR),  
XX hrUP17. The endogenous and non-endogenous, constitutively activated  
XX versions of human G-protein coupled receptors (GPCR), are useful for  
XX direct identification of candidate compounds as receptor agonists,  
XX inverse agonists or partial agonists having applicability as therapeutic  
XX agents for treating diseases related to GPCR, e.g. lung cancer.  
XX Non-endogenous version of human GPCRs are also utilized in research  
XX settings and in vitro and in vivo system, incorporating GPCRs can be  
XX utilised to elucidate and understand the roles these receptors  
XX play in the human condition, both normal and diseased.  
XX  
SQ Sequence 322 AA;  
Query Match 100.0%; Score 1661; DB 22; Length 322;  
Best Local Similarity 100.0%; Pred. No. 4e-171;  
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPITSTLDTLPTINGTEETLCYKQTLSTLVLTCTIVSLVGTGNAVAVMLLGCGRMRNA 60  
DB 1 MDPITSTLDTLPTINGTEETLCYKQTLSTLVLTCTIVSLVGTGNAVAVMLLGCGRMRNA 60  
QY 61 FSIYILNLAADFLFLSGRLIYSLISFISIPHTISKILYPVMWFSYFAGLSFSAVSTER 120  
DB 61 FSIYILNLAADFLFLSGRLIYSLISFISIPHTISKILYPVMWFSYFAGLSFSAVSTER 120  
QY 121 CLSVLMPWYRCHRPHTLSAVVAVCVLLMALSLRSLLEWMLCGFLPSGADSAMCQTSDFIT 180  
DB 121 CLSVLMPWYRCHRPHTLSAVVAVCVLLMALSLRSLLEWMLCGFLPSGADSAMCQTSDFIT 180  
QY 181 VAMLIPLCVVLCGSSIVLLIRILCGSRKIPLTRLYVTITLVVFLVLCGLPGIOFPLFL 240  
DB 181 VAMLIPLCVVLCGSSIVLLIRILCGSRKIPLTRLYVTITLVVFLVLCGLPGIOFPLFL 240

QY 241 WIHVDREVLFCCHVHVSIFLSALNSSANPIYFVGSFRORONRMLKVLQALADASE 300  
 DB 241 WIHVDREVLFCCHVHVSIFLSALNSSANPIYFVGSFRORONRMLKVLQALADASE 300  
 QY 301 VDEGGQGLPEEIIELSGSRLEQ 322  
 DB 301 VDEGGQGLPEEIIELSGSRLEQ 322

## RESULT 3

AAG64294  
 ID AAG64294 standard; Protein; 322 AA.  
 XX  
 AC AAG64294;  
 XX  
 DT 21-SEP-2001 (first entry)  
 XX

XX Human GTP-binding protein-coupled receptor GPRV20.  
 XX

XX GTP-binding protein-coupled receptor; neuroprotective; immunomodulatory;  
 KW muscular; urinary; circulatory; anorectic; human; guanosine triphosphate;  
 KW G-protein.  
 XX

XX Homo sapiens.  
 OS

XX MO200148189-A1.  
 PN

XX 05-JUL-2001.  
 PD

XX 28-DEC-2000; 2000MO-JP09409.  
 PF

XX 28-DEC-1999; 99JP-0375152.  
 PR

XX 31-MAR-2000; 2000JP-0101339.  
 PR

XX 23-MAY-2000; 2000JP-0155978.  
 PR

XX (HELI-) HELIX RES INST.  
 PA

XX Matsumoto S, Oda T, Saico Y, Morikawa N, Yoshida K, Suwa M;  
 PI Sugiyama T;  
 PI

XX WPI; 2001-425663/45.  
 DR

XX N-PSDB; AAA49507.  
 DR

XX Family of guanosine triphosphate binding protein coupled receptors and  
 PT genes encoding them for treatment and prevention of diseases associated  
 PT with these receptors -

XX Claim 1; Pages 75-78; 137pp; Japanese.  
 PS

XX The present sequence is the protein sequence for a human guanosine  
 CC triphosphate (GTP)-binding protein-coupled receptor. The receptor is  
 CC useful for the investigation, diagnosis, treatment and prevention of  
 CC diseases associated with GTP-binding protein-coupled receptors, including  
 CC neurological, circulatory, digestive system, immune system, muscle and  
 CC urinary system disorders. GTP-binding proteins are also known as  
 CC G-proteins.  
 CC

XX Sequence 322 AA;  
 SQ

Query Match 100.0%; Score 1661; DB 22; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 4e-171;  
 Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPTISTLDTELPINGTEETLCYKOTLSLTVLCTIVSLVGTGNNAVVLMLGCRMRNA 60  
 DB 1 MDPTISTLDTELPINGTEETLCYKOTLSLTVLCTIVSLVGTGNNAVVLMLGCRMRNA 60

QY 61 FSIYIINLAADFLISGRILYSLSFISIPHTISKILYPMVMSYPAGSFLSAVSTER 120  
 DB 61 FSIYIINLAADFLISGRILYSLSFISIPHTISKILYPMVMSYPAGSFLSAVSTER 120

QY 121 CLSVLMPIWIRCHRPHTLSAVVCVLLMAISLRSILEMMLCGFLPSGADSAMCQTSDFIT 180  
 DB 121 CLSVLMPIWIRCHRPHTLSAVVCVLLMAISLRSILEMMLCGFLPSGADSAMCQTSDFIT 180

DB 121 CLSVLMPIWIRCHRPHTLSAVVCVLLMAISLRSILEMMLCGFLPSGADSAMCQTSDFIT 180  
 QY 181 VAMILFLCVVLCSSSLVLLIRILCGSRKIPLTRLYVTITLLTVLFLCGLPFGIQEFL 240  
 DB 181 VAMILFLCVVLCSSSLVLLIRILCGSRKIPLTRLYVTITLLTVLFLCGLPFGIQEFL 240  
 QY 241 WIHVDREVLFCCHVHVSIFLSALNSSANPIYFVGSFRORONRMLKVLQALADASE 300  
 DB 241 WIHVDREVLFCCHVHVSIFLSALNSSANPIYFVGSFRORONRMLKVLQALADASE 300  
 QY 301 VDEGGQGLPEEIIELSGSRLEQ 322  
 DB 301 VDEGGQGLPEEIIELSGSRLEQ 322

## RESULT 4

AAE21288  
 ID AAE21288 standard; Protein; 322 AA.  
 XX  
 AC AAE21288;  
 XX

XX 01-JUL-2002 (first entry)  
 DT

XX Human MrgX1 (mas-related gene) protein.  
 DE

XX Human; mas-related gene; G-protein coupled receptor; drug-12 protein;  
 KW receptor; sensory perception; pain; analgesic; MrgX1.  
 KW

XX Homo sapiens.  
 OS

XX MO200183555-A2.  
 PN

XX 08-NOV-2001  
 PD

XX 04-MAY-2001; 2001MO-US14519.  
 PF

XX 04-MAY-2000; 2000US-202027P.  
 PR

XX 01-AUG-2000; 2000US-222344P.  
 PR

XX 03-NOV-2000; 2000US-0704707.  
 PR

XX 19-APR-2001; 2001US-285493P.  
 PR

XX (CALY) CALIFORNIA INST OF TECHNOLOGY.  
 PA

XX Anderson DJ, Dong X, Zylka M, Han S, Simon M;  
 PI WPI; 2002-171346/22.  
 PI

XX N-PSDB; AAD33744.  
 DR

XX Isolated polypeptide, Mrg, which is a G-protein coupled receptor and an  
 PT isolated polypeptide, drug-12, which is also a receptor, useful for  
 PT identifying agonists or antagonists for treating pain -

XX Claim 16; Fig 1; 185pp; English.  
 PS

XX The invention relates to Mrg (mas-related gene) protein, which is a  
 CC G-protein coupled receptor and drug-12 protein, which is a receptor. The  
 CC invention is useful for identifying compounds that bind to it, especially  
 CC agonists or antagonists. Administration of an agent (e.g. the identified  
 CC agonist) that increases the expression of Mrg in a mammal may be used for  
 CC treating impaired sensory perception in a mammal, especially pain. The  
 CC antagonist may also be useful for treating impaired sensory perception in  
 CC a mammal. The present sequence is human MrgX1 protein.  
 CC

XX Sequence 322 AA;  
 SQ

Query Match 100.0%; Score 1661; DB 23; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 4e-171;  
 Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPTISTLDTELPINGTEETLCYKOTLSLTVLCTIVSLVGTGNNAVVLMLGCRMRNA 60  
 DB 1 MDPTISTLDTELPINGTEETLCYKOTLSLTVLCTIVSLVGTGNNAVVLMLGCRMRNA 60

QY 61 FSIYIINLAADPLFLSGRIYLSLSTISIPHTISKILYVPMVMSYFAGISFLSAVSTER 120  
 DB 61 FSIYIINLAADPLFLSGRIYLSLSTISIPHTISKILYVPMVMSYFAGISFLSAVSTER 120  
 QY 121 CLSTVMPWIRCHRPHTLSAVCVLLMALSLSLIEMMLCGFLFGADSAMCQTSDFIT 180  
 DB 121 CLSTVMPWIRCHRPHTLSAVCVLLMALSLSLIEMMLCGFLFGADSAMCQTSDFIT 180  
 QY 181 VAMLIPLCVLCCSSVLVLRILICGSRKIPLTRLYVTLLTVLVLGCLPGIQLPFL 240  
 DB 181 VAMLIPLCVLCCSSVLVLRILICGSRKIPLTRLYVTLLTVLVLGCLPGIQLPFL 240  
 QY 241 WIHVDREVLFCVHLVLSIFLSALNSSANPITTFVGSFRORONKLVQLQALODASE 300  
 DB 241 WIHVDREVLFCVHLVLSIFLSALNSSANPITTFVGSFRORONKLVQLQALODASE 300  
 QY 301 VDEGGGQLPERILSLSGSRLEQ 322  
 DB 301 VDEGGGQLPERILSLSGSRLEQ 322

RESULT 5  
 ID AAE17074 standard; Protein; 322 AA.  
 AC AAE17074;  
 XX  
 XX  
 DT 18-APR-2002 (first entry)  
 XX  
 DE Human G-protein coupled receptor (GPCRx5) protein.  
 XX  
 XX Human, G-protein coupled receptor; GPCR5; cerebroprotective; vomiting;  
 KM receptor-mediated disorder; therapy; urinary retention; allergy; obesity;  
 KM osteoporosis; angina pectoris; restenosis; atherosclerosis; hypertension;  
 KM anorexia; tumour; migraine; acute heart failure; ulcer; antiinflammatory;  
 KM stroke; hypertension; neuronal disorder; myocardial infarction psychotic;  
 KM depression; mental retardation; neurodegenerative disease; antibacterial;  
 KM Alzheimer's disease; dementia; ischaemia; Parkinson's disease; antiviral;  
 KM Huntington's disease; anxiety; antifungal; immunosuppressive; cytostatic;  
 KM vulvarexy; anorectic; anabolic; diuretic; cardiac; neurotropic;  
 KM antileptic; vasotropic; diabetes; cancer; tranquilizer; neuroleptic.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Domain 28..52  
 FT /note= "Transmembrane domain"  
 FT 60..88  
 FT /note= "Transmembrane domain"  
 FT 97..116  
 FT /note= "Transmembrane domain"  
 FT 140..160  
 FT /note= "Transmembrane domain"  
 FT 178..200  
 FT /note= "Transmembrane domain"  
 FT 255..275  
 FT /note= "Transmembrane domain"  
 FT Domain  
 PN WO200198330-A2.  
 XX  
 XX 27-DEC-2001.  
 PD  
 XX  
 PF 20-JUN-2001; 2001MO-BE00104.  
 XX  
 XX 20-JUN-2000; 2000US-212913P.  
 PR 11-JUL-2000; 2000US-217494P.  
 PR 26-JAN-2001; 2001EP-0870015.  
 PR 12-FEB-2001; 2001EP-0870024.  
 XX  
 XX (EURO-) EUROSCREEN SA.  
 PA  
 XX  
 PI Lannoy V, Brezillon S, Dethaux M, Parmentier M, Govarts C;  
 XX

DR MPI: 2002-130789/17.  
 DR N-PSDB; AAD27494.  
 XX  
 XX New G-protein coupled receptor, useful in the manufacture of  
 PT medicaments for treating receptor mediated disorders e.g. acute heart  
 PT failure and Alzheimer's disease  
 XX  
 PS Disclosure, Page 23; 46pp; English.

CC The present invention relates to a G-protein coupled receptor (GPCR) and  
 CC nucleotide encoding it. GPCR are useful in the manufacture of a  
 CC medicament for the prevention and/or treatment of receptor-mediated  
 CC disorders e.g. viral infections, virus and bacterial diseases, diseases  
 CC and disorders involving disturbances of cell migration, development of tumours  
 CC and perturbations of immune system including cancers, development of tumours  
 CC and tumour metastasis, inflammatory and neoplastic processes, bacterial  
 CC and fungal infections, in wound and bone healing, dysfunction of  
 CC regulatory growth functions; pain, diabetes, obesity, anorexia, bulimia,  
 CC urinary retention, osteoporosis, angina pectoris, atherosclerosis, or loss  
 CC restenosis, diseases involving excessive or reduced proliferation or loss  
 CC of smooth muscle cells, aneurysm, stroke, ischaemia, ulcers, allergies,  
 CC benign prostatic hypertrophy, migraine, vomiting; blood circulating  
 CC affections including acute heart failure, hypotension, hypertension and  
 CC myocardial infarction psychologic; neuronal disorders such as anxiety, severe  
 CC schizophrenia, manic depression, depression, delirium, dementia, severe  
 CC mental retardation; degenerative diseases; neurodegenerative diseases  
 CC such as Alzheimer's disease, Parkinson's disease; and dyskinesias e.g.  
 CC Huntington's disease or Gilles de la Tourette's syndrome and other  
 CC related diseases. The present sequence is GPCR5 protein.  
 CC  
 XX  
 XX Sequence 322 AA;  
 SQ  
 Query Match 100.0%; Score 1661; DB 23; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 4e-171;  
 Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPTISTLDTLPINGTEBTLCKYKOTLSITVITCVSLVGLTGNVVMVLMGCRMRRNA 60  
 DB 1 MDPTISTLDTLPINGTEBTLCKYKOTLSITVITCVSLVGLTGNVVMVLMGCRMRRNA 60  
 QY 61 FSIYIINLAADPLFLSGRIYLSLSTISIPHTISKILYVPMVMSYFAGISFLSAVSTER 120  
 DB 61 FSIYIINLAADPLFLSGRIYLSLSTISIPHTISKILYVPMVMSYFAGISFLSAVSTER 120  
 QY 121 CLSTVMPWIRCHRPHTLSAVCVLLMALSLSLIEMMLCGFLFGADSAMCQTSDFIT 180  
 DB 121 CLSTVMPWIRCHRPHTLSAVCVLLMALSLSLIEMMLCGFLFGADSAMCQTSDFIT 180  
 QY 181 VAMLIPLCVLCCSSVLVLRILICGSRKIPLTRLYVTLLTVLVLGCLPGIQLPFL 240  
 DB 181 VAMLIPLCVLCCSSVLVLRILICGSRKIPLTRLYVTLLTVLVLGCLPGIQLPFL 240  
 QY 241 WIHVDREVLFCVHLVLSIFLSALNSSANPITTFVGSFRORONKLVQLQALODASE 300  
 DB 241 WIHVDREVLFCVHLVLSIFLSALNSSANPITTFVGSFRORONKLVQLQALODASE 300  
 QY 301 VDEGGGQLPERILSLSGSRLEQ 322  
 DB 301 VDEGGGQLPERILSLSGSRLEQ 322

RESULT 6  
 ID AAY30162 standard; Protein; 322 AA.  
 XX  
 XX AAY30162;  
 AC  
 XX  
 DT 26-NOV-1999 (first entry)  
 XX  
 DE Human dorsal root receptor 4 HDRR4.  
 XX  
 XX Dorsal root receptor; dorsal root ganglia; G-protein coupled receptor;  
 KM HDRR4; central nervous system; CNS; anaesthesia; analgesia; neuron; pain.



```
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 310
XX FT /note= "Encoded by GAC"
XX FT Misc-difference 312
XX FT /note= "Encoded by ATC"
XX PN W09932519-A1.
XX PD 01-JUL-1999.
XX PF 16-DEC-1998; 98MO-SE02348.
XX PR 22-DEC-1997; 97SE-0004836.
XX PA (ASTR ) ASTRA AB.
XX PA (ASTR-) ASTRA PHARMA INC.
XX PI Ahmad S, Banville D, Fortin Y, Lembo P, O'Donnell D,
XX PI Shen S;
XX DR WPI; 1999-405162/34.
XX DR N-PSDB; AA210070.
XX PT Rat and human dorsal root receptors and related polynucleotides,
XX PT useful for identifying agents for anaesthesia and analgesia
XX PS Claim 21; Page 52-54; 72pp; English.
XX CC This is the human dorsal root receptor 4 (hDRR4) protein sequence. This
XX CC is a G protein coupled receptor that is expressed preferentially in
XX CC dorsal root ganglia. hDRR4 can be used to create antibodies against
XX CC hDRR4. The dorsal root ganglia area of the central nervous system (CNS)
XX CC is densely innervated with primary or afferent neurons involved in
XX CC transmission, modulation and sensation of pain. The DR's which are
XX CC expressed in this region of the CNS may be used for assays for the
XX CC identification of new agents for anaesthesia and analgesia.
XX SQ Sequence 322 AA;
XX
XX Query Match 99.5%; Score 1652; DB 20; Length 322;
XX Best Local Similarity 99.1%; Pred. No. 3,7e-170;
XX Matches 319; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 MDPTISTLDTLTPINGTEETLCYKQTLSTVLTCTIVSLVGLTGNNAVIMLLGCRMRNA 60
XX DB 1 MDPTVSTLDTLTPINGTEETLCYKQTLSTVLTCTIVSLVGLTGNNAVIMLLGCRMRNA 60
XX
XX QY 61 FSIYIINLAADFLFSGRLIYSLFSISIPHTISKILYPMWMSYFAGLSFSAVSTER 120
XX DB 61 FSIYIINLAADFLFSGRLIYSLFSISIPHTISKILYPMWMSYFAGLSFSAVSTER 120
XX
XX QY 121 CLSVLPIMWYRCHRPHTLSAVVCLLMALSLRSILEMMLCGFLFSGADSAMCQTSDFIT 180
XX DB 121 CLSVLPIMWYRCHRPHTLSAVVCLLMALSLRSILEMMLCGFLFSGADSAMCQTSDFIT 180
XX
XX QY 181 VAMLIPLCVLVCSSVLVLRILICGSRKIPLRLYVTITLLTVLVFLCGIPFGIOFFFL 240
XX DB 181 VAMLIPLCVLVCSSVLVLRILICGSRKIPLRLYVTITLLTVLVFLCGIPFGIOFFFL 240
XX
XX QY 241 WIHVREVLFCFHVHVSIFLSALNSSANPIYFVGSFROQRONKIKVLQALQDASE 300
XX DB 241 WIHVREVLFCFHVHVSIFLSALNSSANPIYFVGSFROQRONKIKVLQALQDASE 300
XX
XX QY 301 VDEGGGQLPEETLELSGSRLEQ 322
XX DB 301 VDEGGGQLPEETLELSGSRLEQ 322
XX
XX RESULT 7
XX AAY30161
```

```
ID AAY30161 standard; protein; 322 AA.
XX AC AAY30161;
XX DT 26-NOV-1999 (first entry)
XX DE Human dorsal root receptor 3 hDRR3.
XX KW Dorsal root receptor; dorsal root ganglia; G-protein coupled receptor;
XX KW hDRR3; central nervous system; CNS; anaesthesia; analgesia; neuron; pain.
XX OS Homo sapiens.
XX PN W09932519-A1.
XX PD 01-JUL-1999.
XX PF 16-DEC-1998; 98MO-SE02348.
XX PR 22-DEC-1997; 97SE-0004836.
XX PA (ASTR ) ASTRA AB.
XX PA (ASTR-) ASTRA PHARMA INC.
XX PI Ahmad S, Banville D, Fortin Y, Lembo P, O'Donnell D;
XX PI Shen S;
XX DR WPI; 1999-405162/34.
XX DR N-PSDB; AA210069.
XX PT Rat and human dorsal root receptors and related polynucleotides,
XX PT useful for identifying agents for anaesthesia and analgesia
XX PS Claim 16; Page 48-50; 72pp; English.
XX CC This is the human dorsal root receptor 3 (hDRR3) protein sequence. This
XX CC is a G protein coupled receptor that is expressed preferentially in
XX CC dorsal root ganglia. hDRR3 can be used to create antibodies against
XX CC hDRR3. The dorsal root ganglia area of the central nervous system (CNS)
XX CC is densely innervated with primary or afferent neurons involved in
XX CC transmission, modulation and sensation of pain. The DR's which are
XX CC expressed in this region of the CNS may be used for assays for the
XX CC identification of new agents for anaesthesia and analgesia.
XX SQ Sequence 322 AA;
XX
XX Query Match 97.8%; Score 1624; DB 20; Length 322;
XX Best Local Similarity 97.2%; Pred. No. 4e-167;
XX Matches 313; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 1 MDPTISTLDTLTPINGTEETLCYKQTLSTVLTCTIVSLVGLTGNNAVIMLLGCRMRNA 60
XX DB 1 MDPTVSTLDTLTPINGTEETLCYKQTLSTVLTCTIVSLVGLTGNNAVIMLLGCRMRNA 60
XX
XX QY 61 FSIYIINLAADFLFSGRLIYSLFSISIPHTISKILYPMWMSYFAGLSFSAVSTER 120
XX DB 61 FSIYIINLAADFLFSGRLIYSLFSISIPHTISKILYPMWMSYFAGLSFSAVSTER 120
XX
XX QY 121 CLSVLPIMWYRCHRPHTLSAVVCLLMALSLRSILEMMLCGFLFSGADSAMCQTSDFIT 180
XX DB 121 CLSVLPIMWYRCHRPHTLSAVVCLLMALSLRSILEMMLCGFLFSGADSAMCQTSDFIT 180
XX
XX QY 181 VAMLIPLCVLVCSSVLVLRILICGSRKIPLRLYVTITLLTVLVFLCGIPFGIOFFFL 240
XX DB 181 VAMLIPLCVLVCSSVLVLRILICGSRKIPLRLYVTITLLTVLVFLCGIPFGIOFFFL 240
XX
XX QY 241 WIHVREVLFCFHVHVSIFLSALNSSANPIYFVGSFROQRONKIKVLQALQDASE 300
XX DB 241 WIHVREVLFCFHVHVSIFLSALNSSANPIYFVGSFROQRONKIKVLQALQDASE 300
XX
XX QY 301 VDEGGGQLPEETLELSGSRLEQ 322
XX DB 301 VDEGGGQLPEETLELSGSRLEQ 322
XX
```

## RESULT 8

AAAB14846 standard; Protein, 322 AA.

AC AAB14846;

XX 19-DEC-2000 (first entry)

DE Human novel G-protein coupled receptor #1.

XX Human; novel G-protein coupled receptor; signal transduction;  
KM disease diagnosis; drug screening; disease therapy.

OS Homo sapiens.

XX W0200040724-A1.

XX 13-JUL-2000.

XX 04-JAN-2000; 2000MO-US00052.

XX 04-JAN-1999; 99US-0114666.

XX 14-JAN-1999; 99US-0115828.

XX (LEXI-) LEXICON GENETICS INC.

XX Nehls M, Mattler F;

XX WPI; 2000-465986/40.

XX N-PSDB; AAA70342.

XX New polynucleotides encoding novel G-protein coupled receptors useful  
PT for diagnosis, drug screening, clinical trial monitoring and for the  
PT treatment of physiological or behavioural disorders -

XX Claim 1; Page 53-54; 61pp; English.

XX The present sequence is the protein sequence for a novel human G-protein  
CC coupled receptor (NGPCR). These proteins are involved in signal  
CC transduction pathways in many cases. The protein contains seven  
CC transmembrane domains, and is expressed in human testis, mammary gland  
CC and salivary gland tissue. The protein, its gene, agonists, antagonists  
CC and antibodies can be used to diagnose and treat diseases associated  
CC with the inappropriate expression or expression of mutant versions of the  
CC protein, for screening for drugs which can be used in the same manner,  
CC and for elucidating the function of the protein.

XX Sequence 322 AA;

XX Query Match 83.7%; Score 1390; DB 21; Length 322;

XX Best Local Similarity 83.9%; Pred. No. 8.3e-142;

XX Matches 270; Conservative 16; Mismatches 36; Indels 0; Gaps 0;

XX 1 MDPTSTLDELTPINGTEETLCYKQTLSTLVLCIYSLVGLTGNAAVVMILGCRMRNA 60

XX 1 MDSTIPVGLTETLPINGREETPCYKQTLSTGLTCIYSLVGLTGNAAVVMILGCRMRNA 60

XX 61 FSIYIILNLAADFLFLSGRLIYSLISFISIPHTISKILYPMVMSFYAGLSFSAVSTER 120

XX 61 VSIYIILNLAADFLFLSGRLIYSLISFISIPHTISKILYPMVMSFYAGLSFSAVSTER 120

XX 121 CLSVLMPWIRCHRPETHLSAVVAVVILMALSLRSLILEMMLCGPLFGADSAWCQTSDFIT 180

XX 121 CUSIIMPIWYHCRBRPYLSSVMCVLIMLRLSLILEMMLCGPLFGADSAWCQTSDFIT 180

XX 181 VAMIELCVYLGGSSIVLIRILGSRKIPLRVAVTILLVAVPLGSLPGIQPFL 240

XX 181 IAMLVFLCVLGGSSIVLIRILGSRKIPLRVAVTILLVAVPLGSLPGIQPFL 240

XX 241 WIVHREVLFCHVHLSIFLSALNSANPIYFVGSFRQNRQNLKVLQALQDASE 300

DB 241 RIHLDMKVLFCVHVLVIFLSALNSANPIYFVGSFRQNRQNLKVLQALQDTPB 300

XX 301 VDEGGQLPEETLELSGRLEQ 322

DB 301 VDEGGQLPEETLELSGRLEQ 322

## RESULT 9

AAAY90761 standard; Protein, 322 AA.

XX AAY90761;

XX 18-AUG-2000 (first entry)

XX Human G protein-coupled receptor hHR7213 SEQ ID NO:1.

XX Human; G protein-coupled receptor; hippocampus; diagnosis; screening;

XX genetic disease; cellular function regulation.

XX Homo sapiens.

XX W0200020455-A1.

XX 13-APR-2000.

XX 30-SEP-1999; 99MO-JP05366.

XX 01-OCT-1998; 98JP-0279535.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Watanabe T, Terao Y, Matsui H;

XX WPI; 2000-303747/26.

XX N-PSDB; AAA29811.

XX Human-derived G protein-coupled protein and encoding nucleic acid,  
PT useful e.g. in determining ligands and treatment of diseases associated  
PT with dysfunction of the protein -

XX Claim 1; Page 90-91; 97pp; Japanese.

XX The present sequence represents a human-derived G protein-coupled protein  
CC designated hHR7213, which is isolated from the human hippocampus.  
CC The G protein-coupled receptor can be used for preventing, treating and  
CC diagnosing genetic diseases associated with G protein-coupled protein,  
CC and for regulating cellular functions. The protein can be used to  
CC prevent and treat disorders associated with G protein-coupled protein  
CC gene dysfunction. It can also be used to identify G protein-coupled  
CC protein ligands and generating antibodies and antisera against the  
CC protein. It is also useful in constructing recombinant receptor protein  
CC expression systems, developing receptor-binding assay systems and  
CC screening drug candidates, and can be used as a probe in the genetic  
CC diagnosis of G protein-coupled protein disorders.

XX Sequence 322 AA;

XX Query Match 83.3%; Score 1383; DB 21; Length 322;

XX Best Local Similarity 83.5%; Pred. No. 4.7e-141;

XX Matches 269; Conservative 16; Mismatches 37; Indels 0; Gaps 0;

XX 1 MDPTSTLDELTPINGTEETLCYKQTLSTLVLCIYSLVGLTGNAAVVMILGCRMRNA 60

XX 1 MDSTIPVGLTETLPINGREETPCYKQTLSTGLTCIYSLVGLTGNAAVVMILGCRMRNA 60

XX 61 FSIYIILNLAADFLFLSGRLIYSLISFISIPHTISKILYPMVMSFYAGLSFSAVSTER 120

XX 61 VSIYIILNLAADFLFLSGRLIYSLISFISIPHTISKILYPMVMSFYAGLSFSAVSTER 120

XX 121 CLSVLMPWIRCHRPETHLSAVVAVVILMALSLRSLILEMMLCGPLFGADSAWCQTSDFIT 180

XX 121 CUSIIMPIWYHCRBRPYLSSVMCVLIMLRLSLILEMMLCGPLFGADSAWCQTSDFIT 180

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QY 181 VAMLIPLCVLCCSSLVLLIRILCGSRKIPITRLVYITLITVAVFLCGLPFGIOFPL 240
DB 181 IAWLVFLCVLCCSSLVLLIRILCGSRKMPITRLVYITLITVAVFLCGLPFGIOFPL 240
QY 241 WIHVDREVLFCCHVLVSIPLSALNSSANPIITFFVGSFRORONKLVORALDASE 300
DB 241 RIHDMKVLFCCHVLVSIPLSALNSSANPIITFFVGSFRORONKLVORALDASE 300
QY 301 VDEGGGQLPEEILSLGSRLEQ 322
DB 301 VDEGGGWLPEETELSGSRLEQ 322

RESULT 10
AAE21296
ID AAE21296 standard; Protein; 322 AA.
AC AAE21296;
XX
XX 01-JUL-2002 (first entry)
DE Human MrgX3 (mas-related gene) protein.
XX
XX Human; mas-related gene; G-protein coupled receptor; drg-12 protein;
KM receptor; sensory perception; pain; analgesic; MrgX3.
XX
XX Homo sapiens.
XX
XX W020018355-A2.
XX
XX 08-NOV-2001.
XX
XX 04-MAY-2001; 2001MO-US14519.
XX
XX 04-MAY-2000; 2000US-202027P.
PR 01-AUG-2000; 2000US-222344P.
PR 03-NOV-2000; 2000US-0704707.
PR 19-APR-2001; 2001US-285493P.
XX
XX (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
XX Anderson DJ, Dong X, Zylka M, Han S, Simon M;
PI
XX WPI: 2002-171346/22.
DR N-PSDB; AAD33751.
XX
XX Isolated polypeptide, Mrg, which is a G-protein coupled receptor and an
PT isolated polypeptide, drg-12, which is also a receptor, useful for
XX identifying agonists or antagonists for treating pain -
XX
XX Claim 16; Page 130; 185pp; English.
XX
XX The invention relates to Mrg (mas-related gene) protein, which is a
CC G-protein coupled receptor and drg-12 protein, which is a receptor. The
CC invention is useful for identifying compounds that bind to it, especially
CC agonists or antagonists. Administration of an agent (e.g. the identified
CC agonist) that increases the expression of Mrg in a mammal may be used for
CC treating impaired sensory perception in a mammal, especially pain. The
CC antagonist may also be useful for treating impaired sensory perception in
CC a mammal. The present sequence is human MrgX3 protein.
XX
XX Sequence 322 AA;
SQ
Query Match 83.3%; Score 1383; DB 23; Length 322;
Best Local Similarity 83.3%; Pred. No. 4.7e-141;
Matches 269; Conservative 16; Mismatches 37; Indels 0; Gaps 0;
QY 1 MDPTISTLTDELTPINGTEETFLCYKQTLSTLTLCIVSLVGLTGNNAVLMILGCRMRNA 60
DB 1 MDSITIPVLGTEITPINGREETPCPKQTLSTLTLCIVSLVGLTGNNAVLMILGCRMRNA 60
QY 61 FSIYIILMAADFLPLSGRLIYSLSPISIPHTISKILYPMVMSYPAGLSFSAVSTER 120

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DB 61 VSIYIILMAADFLPLSGRLIYSLSPISIPHTISKILYPMVMSYPAGLSFSAVSTER 120
QY 121 CLSLVPIWYRCRPHLSAIVCVLLMALSLRSILEMMLCGFLFGADSAMCOTSDPIT 180
DB 121 CLSLVPIWYRCRPHLSAIVCVLLMALSLRSILEMMLCGFLFGADSAMCOTSDPIT 180
QY 181 VAMLIPLCVLCCSSLVLLIRILCGSRKIPITRLVYITLITVAVFLCGLPFGIOFPL 240
DB 181 IAWLVFLCVLCCSSLVLLIRILCGSRKMPITRLVYITLITVAVFLCGLPFGIOFPL 240
QY 241 WIHVDREVLFCCHVLVSIPLSALNSSANPIITFFVGSFRORONKLVORALDASE 300
DB 241 RIHDMKVLFCCHVLVSIPLSALNSSANPIITFFVGSFRORONKLVORALDASE 300
QY 301 VDEGGGQLPEEILSLGSRLEQ 322
DB 301 VDEGGGWLPEETELSGSRLEQ 322

RESULT 11
AAU97598
ID AAU97598 standard; Protein; 337 AA.
AC AAU97598;
XX
XX 12-AUG-2002 (first entry)
DE Human G-protein coupled receptor (GPCR).
XX
XX Human; G-protein coupled; receptor; GPCR; human prolase;
KM human therapeutic protein; query sequence; search; chromosome 3;
XX sequence database; non-human transgenic animal; gene therapy.
XX
XX Homo sapiens.
XX
XX Location/Qualifiers
FH Key 41..61
FT Domain /label= Helix_1
FT 75..95
FT Domain /label= Helix_2
FT 112..132
FT Domain /label= Helix_3
FT 133..135
FT Modified-site /note="Protein kinase C (PKC) phosphorylation site"
FT 151..171
FT Domain /label= Helix_4
FT 169..172
FT Modified-site /note="Casein kinase II (CK2) phosphorylation site"
FT 181..184
FT Modified-site /note="Casein kinase II (CK2) phosphorylation site"
FT 193..213
FT Domain /label= Helix_5
FT 221..223
FT Modified-site /note="Protein kinase C (PKC) phosphorylation site"
FT 229..249
FT Domain /label= Helix_6
FT 244..249
FT Modified-site /note="Myristoylation site"
FT 248..253
FT Modified-site /note="Myristoylation site"
FT 261..281
FT Domain /label= Helix_7
FT 279..282
FT Modified-site /note="Asn glycosylation site"
FT 292..294
FT Modified-site /note="Protein kinase C (PKC) phosphorylation site"
FT 333..336
FT Modified-site /note="Casein kinase II (CK2) phosphorylation site"
XX
XX W0200234914-A1.
XX
XX 02-MAY-2002.

```

XX 10-OCT-2001; 2001MO-US1592.  
XX  
XX 25-OCT-2000; 2000US-0695045.  
XX 31-MAY-2001; 2001US-0867570.  
XX  
XX (PEKE ) PE CORP NY.  
XX  
XX Wei M, Zhao Q, Woodage T, Di Francesco V, Beasley EM,  
XX  
XX WPI; 2002-463360/49.  
XX  
XX N-PSDB; ABK52822, ABK52823.  
XX  
XX Novel isolated G-protein coupled receptor peptide useful for treating  
XX disorder characterised by absence of inappropriate or unwanted  
XX expression of the receptor protein, and as immunogens to raise  
XX antibodies -  
XX  
XX Claim 1; Fig 2; 75pp; English.  
XX  
XX The present invention relates to a new G-protein coupled receptor  
XX (GPCR) peptide. The invention is useful for identifying a modulator  
XX of GPCR and for treating a disease or condition mediated by a human  
XX protease. The invention is also useful as models for the development  
XX of human therapeutics, for identifying therapeutic proteins, as  
XX targets for development of human therapeutic agents, and as query  
XX sequence to perform a search against sequence databases to, for  
XX e.g., identify other family members of related sequences. The  
XX vector of the invention is useful for producing a GPCR protein or  
XX peptide, for conducting cell-based assays involving the GPCR protein  
XX or its fragment, for identifying GPCR protein mutants whose  
XX functions are affected, and to produce non-human transgenic animals.  
XX The present amino acid sequence represents the human G-protein  
XX coupled receptor (GPCR) protein of the invention. This sequence is  
XX encoded by the human G-protein coupled receptor (GPCR) gene located  
XX on chromosome 3.  
XX  
XX Sequence 337 AA;  
SQ  
Query Match 83.3%; Score 1383; DB 23; Length 337;  
Best local similarity 83.5%; Pred. No. 5e-14;  
Matches 269; Conservative 16; Mismatches 37; Indels 0; Gaps 0;  
QY 1 MDPTISTLTDELTPINGTEETLCYKQTLSTVLTCTVSLVGLTGNVAVMLLGCRRRNA 60  
DB 16 MDSTIPVLGTETLPINGRETPCYKQTLSTGLTCTVSLVGLTGNVAVMLLGCRRRNA 75  
QY 61 FSIYIINLAADFLFLSGRLIYSLISFISIPHTISKILYVVMFVSFAGLSFLSAVSTER 120  
DB 76 VSIYIINLAADFLFLSGRLIYSLISFISIPHTISKILYVVMFVSFAGLSFLSAVSTER 135  
QY 121 CLSVLMPWYRCHRPHTLSAVCVLLMALSLRSILEMMLCGFLFGSADSAMQOTDFT 180  
DB 136 CLSTIMPIWYCHRRPHTLSAVCVLLMALSLRSILEMMLCGFLFGSADSAMQOTDFT 195  
QY 181 VAMLIFLCVLCGSSVLVLRILGSRKIPLTRLYVTLLTVVFLLCGLPFGIQPFL 240  
DB 196 IAMLVFLCVLCGSSVLVLRILGSRKIPLTRLYVTLLTVVFLLCGLPFGIQPFL 255  
QY 241 WIHVDREVLFCVHLVSIIFLSALNSSANPIIYFVGSFRORONIKLVLRALODASE 300  
DB 256 RIHDMKVLFCVHLVSIIFLSALNSSANPIIYFVGSFRORONIKLVLRALODASE 315  
QY 301 VDEGGGQLPEETLELSSRLAQ 322  
DB 316 VDEGGGQLPEETLELSSRLAQ 337

RESULT 12  
AA90762  
ID AA90762 standard; Protein; 322 AA.  
XX  
AC AA90762;

XX 18-AUG-2000 (first entry)  
XX  
XX Human G protein-coupled receptor hH17T213V SEQ ID NO:2.  
XX  
XX Human; G protein-coupled receptor; hippocampus; diagnosis; screening;  
XX genetic disease; cellular function regulation.  
XX  
XX Homo sapiens.  
XX  
XX WO200020455-A1.  
XX  
XX 13-APR-2000.  
XX  
XX 30-SEP-1999; 99WO-JP05366.  
XX  
XX 01-OCT-1998; 98JP-0279535.  
XX  
XX (TAKEDA ) TAKEDA CHEM IND LTD.  
XX  
XX Watanabe T, Terao Y, Matsui H;  
XX  
XX WPI; 2000-303747/26.  
XX  
XX N-PSDB; AAA29812.  
XX  
XX Human-derived G protein-coupled protein and encoding nucleic acid,  
XX useful e.g. in determining ligands and treatment of diseases associated  
XX with dysfunction of the protein -  
XX  
XX Claim 2; Page 92-93; 97pp; Japanese.  
XX  
XX The present sequence represents a human-derived G protein-coupled protein  
XX designated hH17T213V, which is isolated from the human hippocampus.  
XX The G protein-coupled receptor can be used for preventing, treating, and  
XX diagnosing genetic diseases associated with G protein-coupled protein,  
XX and for regulating cellular functions. The protein can be used to  
XX prevent and treat disorders associated with G protein-coupled protein  
XX gene dysfunction. It can also be used to identify G protein-coupled  
XX protein ligands and generating antibodies and antisera against the  
XX protein. It is also useful in constructing recombinant receptor protein  
XX expression systems, developing receptor-binding assay systems and  
XX screening drug candidates, and can be used as a probe in the genetic  
XX diagnosis of G protein-coupled protein disorders.  
XX  
XX Sequence 322 AA;  
SQ  
Query Match 83.0%; Score 1378; DB 21; Length 322;  
Best local similarity 83.2%; Pred. No. 1.6e-140;  
Matches 268; Conservative 17; Mismatches 37; Indels 0; Gaps 0;  
QY 1 MDPTISTLTDELTPINGTEETLCYKQTLSTVLTCTVSLVGLTGNVAVMLLGCRRRNA 60  
DB 1 MDSTIPVLGTETLPINGRETPCYKQTLSTGLTCTVSLVGLTGNVAVMLLGCRRRNA 60  
QY 61 FSIYIINLAADFLFLSGRLIYSLISFISIPHTISKILYVVMFVSFAGLSFLSAVSTER 120  
DB 61 VSIYIINLAADFLFLSGRLIYSLISFISIPHTISKILYVVMFVSFAGLSFLSAVSTER 120  
QY 121 CLSVLMPWYRCHRPHTLSAVCVLLMALSLRSILEMMLCGFLFGSADSAMQOTDFT 180  
DB 121 CLSTIMPIWYCHRRPHTLSAVCVLLMALSLRSILEMMLCGFLFGSADSAMQOTDFT 180  
QY 181 VAMLIFLCVLCGSSVLVLRILGSRKIPLTRLYVTLLTVVFLLCGLPFGIQPFL 240  
DB 181 IAMLVFLCVLCGSSVLVLRILGSRKIPLTRLYVTLLTVVFLLCGLPFGIQPFL 240  
QY 241 WIHVDREVLFCVHLVSIIFLSALNSSANPIIYFVGSFRORONIKLVLRALODASE 300  
DB 241 RIHDMKVLFCVHLVSIIFLSALNSSANPIIYFVGSFRORONIKLVLRALODASE 300  
QY 301 VDEGGGQLPEETLELSSRLAQ 322  
DB 301 VDEGGGQLPEETLELSSRLAQ 322

## RESULT 13

AA30159  
ID AAY30159 standard; protein, 322 AA.

XX AAY30159;

DT 26-NOV-1999 (first entry)

XX Human dorsal root receptor 1 hDRR1.

XX Dorsal root receptor; dorsal root ganglia; G-protein coupled receptor;  
KM hDRR1; central nervous system; CNS; anaesthesia; analgesia; neuron; pain.

XX Homo sapiens.

XX MO9932519-A1.

XX 01-JUL-1999.

XX 16-DEC-1998; 98MO-SE02348.

XX 22-DEC-1997; 97SE-0004836.

XX (ASTR ) ASTRA AB.

XX (ASTR-) ASTRA PHARMA INC.

XX Ahmad S, Banville D, Fortin Y, Lembo P, O'Donnell D,  
PI Shen S;

XX WPI; 1999-405162/34.

XX N-PSDB; AA210067.

XX Rat and human dorsal root receptors and related polynucleotides,  
PT useful for identifying agents for anaesthesia and analgesia

XX Claim 6; Page 39-41; 72pp; English.

XX This is the human dorsal root receptor 1 (hDRR1) protein sequence. This  
is a G protein coupled receptor that is expressed preferentially in  
dorsal root ganglia. hDRR1 can be used to create antibodies against  
hDRR1. The dorsal root ganglia area of the central nervous system (CNS)  
is densely innervated with primary or afferent neurons involved in  
transmission, modulation and sensation of pain. The DR's which are  
expressed in this region of the CNS may be used for assays for the  
identification of new agents for anaesthesia and analgesia.

XX Sequence 322 AA;

XX Query Match 82.7%; Score 1373; DB 20; Length 322;

XX Best Local Similarity 82.0%; Pred. No. 5.7e-140; Mismatches 26; Conservative 22; Indels 0; Gaps 0;

XX 1 MDPTISTLDELTPINGTEETLCYKQTLSTVLTCTIVSLVGLTGNAAVLMGLGCRMRNA 60

XX 1 MDPTIPVLGKTLPIINGREETPCYNQTLSTVLTCTIVSLVGLTGNAAVLMGLGCRMRNA 60

XX 61 FSIYIILNLAADPLFLSGRLIYLSLFSISPTISKILYPMVMFSYAGISFLSAVSTER 120

XX 61 VSIYIILNLAADPLFLSGRLIYLSLFSISPTISKILYPMVMFSYAGISFLSAVSTER 120

XX 121 CLSVLWPIWYRCRPHLSAVVAVCVLWALSLRSILEMMLCGFLFGADSAMCOTSDPFT 180

XX 121 CLSVLWPIWYRCRPHLSAVVAVCVLWALSLRSILEMMLCGFLFGADSAMCOTSDPFT 180

XX 181 VAMLIPLCVLCCGSLVLLIRILGSRKIPLTRLYVTITLLTVLVLGCLPFGIOFPLFL 240

XX 181 IAWLVPLCVLCCGSLVLLIRILGSRKIPLTRLYVTITLLTVLVLGCLPFGIOFPLFL 240

XX 241 MIHVDREVLFCGHVLSIFLSALNSSANPIIYFVGSFROKRONKILVORALQDTPE 300

XX 241 RIHDMKVLFCGHVLSIFLSALNSSANPIIYFVGSFROKRONKILVORALQDTPE 300

## RESULT 14

AA87664  
ID AAY87664 standard; protein, 322 AA.

XX AAY87664;

DT 11-AUG-2000 (first entry)

XX Human G protein-coupled receptor protein #2.

XX G protein-coupled receptor protein; human; treatment; diagnosis;  
KM genetic disorder.

XX Homo sapiens.

XX WO200020456-A1.

XX 13-APR-2000.

XX 30-SEP-1999; 99MO-JP05365.

XX 01-OCT-1998; 98JP-0279512.

XX 20-OCT-1998; 98JP-0298667.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Watanabe T, Terao Y, Fukusumi S;

XX WPI; 2000-303748/26.

XX N-PSDB; AAA12208.

XX Novel human-originated G protein-coupled protein and encoding nucleic  
PT acid, useful for e.g. identifying ligands and treating diseases  
PT associated with dysfunction of the protein

XX Claim 2; Page 97-98; 105pp; Japanese.

XX This invention describes a novel human G protein-coupled receptor  
protein (I). The products of the invention can be used for preventing,  
treating and diagnosing gene diseases and for regulating cellular  
functions. The protein can be used to identify ligands and generate  
antibodies and antisera. It is also useful in the construction of a  
CC recombinant receptor protein expression system, developing a  
CC receptor-binding assay system and screening drug candidates and as a  
CC probe in diagnosing genetic disorders involving G protein-coupled  
CC protein. This sequence represents a human G-protein coupled receptor  
CC protein described in the method of the invention.

XX Sequence 322 AA;

XX Query Match 79.1%; Score 1314; DB 21; Length 322;

XX Best Local Similarity 80.6%; Pred. No. 1.4e-133; Mismatches 258; Conservative 20; Indels 0; Gaps 0;

XX 1 MDPTISTLDELTPINGTEETLCYKQTLSTVLTCTIVSLVGLTGNAAVLMGLGCRMRNA 60

XX 1 MDPTIPVLGKTLPIINGREETPCYNQTLSTVLTCTIVSLVGLTGNAAVLMGLGCRMRNA 60

XX 61 FSIYIILNLAADPLFLSGRLIYLSLFSISPTISKILYPMVMFSYAGISFLSAVSTER 120

XX 61 VSIYIILNLAADPLFLSGRLIYLSLFSISPTISKILYPMVMFSYAGISFLSAVSTER 120

XX 121 CLSVLWPIWYRCRPHLSAVVAVCVLWALSLRSILEMMLCGFLFGADSAMCOTSDPFT 180

XX 121 CLSVLWPIWYRCRPHLSAVVAVCVLWALSLRSILEMMLCGFLFGADSAMCOTSDPFT 180

XX 181 VAMLIPLCVLCCGSLVLLIRILGSRKIPLTRLYVTITLLTVLVLGCLPFGIOFPLFL 240

DB 181 VAMLIPLCVLGGSSVLVLRILGSRKMPLTRLYVTILLTVLVLGCLPGIQLALTY 240  
 QY 241 WIHVDREVLFCVHLVSIPLSALNSSANPIIYFVGSFRQRONKLVLRALODASE 300  
 DB 241 RMHNLLEVLYCHVHLVLCVSSLSLSSANPIIYFVGSFRQRONKLVLRALODKPE 300  
 QY 301 VDEGGGOLPEEILIELSGSRL 320  
 DB 301 VDKGBGOLPEESLELSGSRL 320

## RESULT 15

AA30160  
 ID AA30160 standard; protein; 322 AA.

XX AA30160;  
 AC  
 XX  
 DT 26-NOV-1999 (first entry)  
 XX

DE Human dorsal root receptor 2 hDRR2.

XX Dorsal root receptor; dorsal root ganglia; G-protein coupled receptor;  
 KW hDRR2; central nervous system; CNS; anaesthesia; analgesia; neuron; pain.

XX Homo sapiens.

XX WO9932519-A1.

XX 01-JUL-1999.

XX 16-DEC-1998; 98WO-SE02348.

XX 22-DEC-1997; 97SE-0004836.

XX (ASTR-) ASTRA AB.  
 PA (ASTR-) ASTRA PHARMA INC.

XX Ahmad S, Banville D, Fortin Y, Lembo P, O'Donnell D;  
 PI Shen S;

XX WPI; 1999-405162/34.

XX N-PSDB; AA210068.

XX Rat and human dorsal root receptors and related polynucleotides,  
 PT useful for identifying agents for anaesthesia and analgesia

XX Claim 11, Page 43-45; 72pp; English.

XX This is the human dorsal root receptor 2 (hDRR2) protein sequence. This  
 CC is a G protein coupled receptor that is expressed preferentially in  
 CC dorsal root ganglia. hDRR2 can be used to create antibodies against  
 CC hDRR2. The dorsal root ganglia area of the central nervous system (CNS)  
 CC is densely innervated with primary or afferent neurons involved in  
 CC transmission, modulation and sensation of pain. The DRs which are  
 CC expressed in this region of the CNS may be used for assays for the  
 CC identification of new agents for anaesthesia and analgesia.

XX Sequence 322 AA;

Query Match 79.0%; Score 1313; DB 20; Length 322;  
 Best Local Similarity 80.1%; Pred. No. 1.8e-133;  
 Matches 257; Conservative 21; Mismatches 43; Indels 0; Gaps 0;

QY 1 MDPTISTIDTELPINGTEETLCYKQTLSTVLTCIVSLVGLTGNNAVVLMLGGRMRNA 60  
 DB 1 MDPTVPVGTGLTITNGEETPCYKQTLSTGLTCIVSLVGLTGNNAVVLMLGGRMRNA 60  
 QY 61 FSIYIILAAADFLFLSGRLIYSLSPISPHITISKILYPMMSYFAGLSFLSAVSTER 120  
 DB 61 VSIYIILAAADFLFLSGRLIYSLSPISPHITISKILYPMMSYFAGLSFLSAVSTER 120  
 QY 121 CLSVLMPITWYRCHRTHTLSAVVAVLMLSLRSILEMMLCGFLPSGADSNMCTSDFIT 180

DB 121 CISTIMPIWYRCRPRYISSVMCVLMAPSLLRSILEMFCDFLPSGADSVRCETSDFIT 180  
 QY 181 VAMLIPLCVLGGSSVLVLRILGSRKIPLTRLYVTILLTVLVLGCLPGIQLALTY 240  
 DB 181 IAMLVFLRVLGGSSVLVLRILGSRKMPLTRLYVTILLTVLVLGCLPGIQLALTY 240  
 QY 241 WIHVDREVLFCVHLVSIPLSALNSSANPIIYFVGSFRQRONKLVLRALODASE 300  
 DB 241 RIHLDMKVLFCVHLVSIPLSALNSSANPIIYFVGSFRQRONKLVLRALODKPE 300  
 QY 301 VDEGGGOLPEEILIELSGSRL 321  
 DB 301 VDEGGGOLPEEILIELSGSRL 321

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